

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 27, 2003, 08:06:46 ; Search time 4141 Seconds

(without alignments)
2943.991 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQAISPAKFLAGGIAAA.....LRGMCAPVLYLDELKRYI 298

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-UNITS=bits -START=1 -END=1 -MATRIX=bloms62 -TRANS=human40.coi -LIST=45
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-OUTFT=plc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
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Database :

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	897	6 AX134720	AX134720 Sequence
2	1543	100.0	897	6 AX301848	AX301848 Sequence
3	1543	100.0	1193	9 BC008935	BC008935 Homo sapi
4	1543	100.0	1308	9 BC007295	BC007295 Homo sapi
5	1543	100.0	1344	9 AY007135	AY007135 Homo sapi
6	1543	100.0	1366	9 BC007850	BC007850 Homo sapi
7	1543	100.0	1399	9 BC031912	BC031912 Homo sapi
8	1543	100.0	1466	9 BC008737	BC008737 Homo sapi
9	1537	99.6	1455	9 BC014775	BC014775 Homo sapi
10	1512	98.5	1349	4 BOVT27RANS	M24103 Bovine ADP/
11	1474	95.5	1010	5 AB088686	AB088686 Gallus ga
12	1454	94.2	897	6 AX134719	AX134719 Sequence
13	1454	94.2	897	6 AX301847	AX301847 Sequence
14	1454	94.2	1228	9 HUMATPC	J02683 Human ADP/A
15	1451	94.0	1146	4 AB065433	AB065433 Bos tauru
16	1451	94.0	1215	10 RATYANR2	D12771 Rattus norv
17	1446	93.7	1265	5 AF506216	AF506216 Danio rer
18	1445	93.6	897	10 MMT10404	U10404 Mus musculu
19	1445	93.6	1226	10 BC004570	BC004570 Mus muscu
20	1445	93.6	1244	10 BC0027316	BC0027316 Mus muscu
21	1445	93.6	1280	10 MMANTAP	X70847 M. musculus
22	1424	92.3	1196	6 AX401651	AX401651 Sequence
23	1424	92.3	1196	10 RATYANR1	D12770 Rattus norv
24	1422	92.2	932	4 AB009386	AB009386 Oryctolag
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26	1421	92.1	1289	5 AF231347	AF231347 Xenopus l
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40	1402	90.9	1310	5 AB008457	AB008457 Rana rugo
41	1394	90.3	231319	10 AC122916	AC122916 Mus muscu
42	1385.5	89.8	894	6 AX134718	AX134718 Sequence
43	1385.5	89.8	894	6 AX301846	AX301846 Sequence
44	1385.5	89.8	1320	6 AX664496	AX664496 Sequence
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ALIGNMENTS

RESULT 1

AXI34720	AXI34720	897 bp	DNA	linear	PAT 29-MAY-2001
LOCUS	Sequence 3 from Patent WO0132876.				
DEFINITION	AXI34720				
ACCESSION	AXI34720.1				
VERSION	GI:14271237				
KEYWORDS					
SOURCE	homo sapiens (human)				
ORGANISM	homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eultheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Murphy, A.N., Clevenger, W., Wiley, S.E., Andreyev, A.Y., Frigert, L.G., Velickel, G., and Davis, R.E.				
TITLE	Compositions and methods for determining interactions of mitochondrial components, and for identifying agents that alter such interactions				
JOURNAL	Patent: WO 0132876-A 3 10-MAY-2001.				
FEATURES	MITOKOR (US)				
source	Location/Qualifiers				
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ORIGIN					
Alignment Scores:					
Pred. No.:	8.86e-145	Length:	897		
Score:	1543.00	Matches:	298		
Percent Similarity:	100.00%	Conservative:	0		
Best local Similarity:	100.00%	Mismatches:	0		
Query Match:	100.00%	Indels:	0		
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Db	61 ATCTCCAAAGCGCCGCGCTCGATCGAGGGGTCAAGTGGCTGCTCGAGTCCACAC	120			
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Db	181 ATCCCAAGAGAGCGGCGTGTCTCTCTGAGGGGCACCTTCCACAGCTCATTTCCG	240			
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Db	301 GGGGGGCTGACAGACACAGCAGATCTTGGAGATCACTTTCGGGCAACCTGCTCGGC	360			
OY	121 G1ValAlaGlyAlaIrrserIleuCyPheValIlyrProleuAspPheAlaArgThrArg	140			
Db	361 GGTGGCGCGCGGCGACCTCCCTCTCTCGTGGTACCGCGCGGATTTTCCGGAACCGCG	420			
OY	141 IeualAlaAspValaGlylyserGlyTrrhngluArgGluPheArgglyleuGlyAspCys	160			
Db	421 CTGGCAGCGGACGTGGGAAATCGACGACAGACCGCGAGTTCCGAGACCTCGGAGACATGC	480			
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Db	481 CTGTGTAAATATCCCAATCGGAGATCGGGGCTGTACCGAGGCTTCAGTGTCTCC	540			
OY	181 ValGlncllylleIleIrrTrrArgAlaAlaIlyrPheIglyValIlyrAspPrrAlaIysGly	200			

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QY	241	GlnSerGlyArGlyGlyAlaAspIleMetTyrThGlyThValaAPCySTTPArGlys	260
Db	721	CAGTCCGGGGCAAGAGACTGACATCATGTATACACGGACCGCTGCACCTGTGGAGAG	780
QY	261	IlePheArGAspGluGlyGlyValaIaPhePhaGlyValaITPserAnValleuATG	280
Db	781	ATCTTCAGAGATAGGGGGGAGGCGCTCTTCAGGGTGGTGGTCAACGTCTGCGG	840
QY	281	GlyMetGlyAlaPheValleuValleuTyrAspGluIleuIlyGlyValle	298
Db	841	GGCATGGGGGGCGCTTCTGTGGTCTGTACACAGACTCAAGAGGTGATC	894
RESULT 2			
LOCUS	AX301848	897 bp	DNA
DEFINITION	Sequence 3 from Patent WO0185944.		linear
ACCESSION	AX301848		
VERSION	AX301848.1		
KEYWORDS	GI:17382905		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
AUTHORS	Anderson,C.M., Davis,R.E., Clevenger,W., Wiley,S.E., Miller,S.W., Szabo,T.R., Ghosh,S.S., Moos,W.H., Pei,Y. and Carroll,A.K.		
TITLE	Production of adenine nucleotide translocator (ant), novel ant ligands and screening assays therefor		
JOURNAL	Patent: WO 0185944-A 3 15-NOV-2001; MITOKOR (US)		
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BASE COUNT	174 a 274 c 287 g 162 t		
ORIGIN			
Alignment Scores:			
Pred.No.:	8..866-145	Length:	897
Score:	1543.00	Matches:	298
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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QY	21	IleSerLyThAlaValaIaProIleGluArGValYalSleuIleuGlnAlaGlnHis	40
Db	61	ATCTCCAAAGCGCGGTGTGCTCCGATCGACGGGTCAACGTCTGCTGAGCGTCCAGC	120
QY	41	AlaSerLyGlnIleAlaIaAspLyGlnIleTyrLyGlyIleValaAPCySTTPArG	60
Db	121	GCCAGCAAGATGCGCGCGCAACACAGTACAGGCACTGTGAGCTGATGTGCGC	180
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DB 181 ATCCCAAGGAGGAGGCGTGTCTGCTTCCTGAGGGGCAACCTTCCCAAGCTCATTCGC 240

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DB 241 TACTTCCCACTCAAGCCCTCAACTCCGCTTCAAGGATGATGACAGAGATCTTCGCG 300

QY 101 GtYgLYaLaAspLysHisThrGlnPheTTPaTgTyrPheAlaGlyAsnLeuAlaSerGly 120

DB 301 GGGGGCGTGGACACACACGAGTTCGAGGTACTTGGCGGCAACTGGCGCTCCGCGC 360

QY 121 GtYLaLaLaGtLYaLaThrSerLeuGysPheValTyrProLeuAspPheAlaArgThrArg 140

DB 361 GGTGGGGCGGGCGGCACTCTCTGCTTCGTTGATACCCCTTGATTTTCCAGAACCCCGC 420

QY 141 LeuAlaLaAspValGtLYaSerGtLYaThrGtLYaGtLYaPheArgLYaLeuGtLYaSerGly 160

DB 421 CTGGCAGCGGAGCTGGGAAAGTCAGGCAAGAGCGGAGTTCGAGCGCTGGGAGACTGC 480

QY 161 LeuValLysIleThrLysSerAspGtLYaIleArgGtLYaLeuTyrGlnGtLYaPheSerValSer 180

DB 481 CTGGTGAAGATCACCAAGTCCAGCGCATCGGGGCGCTGTACAGGCGCTTCAAGTGTCTCC 540

QY 181 ValGlnGtLYaIleIleLeuTyrArgAlaIaTyrPheGtLYaValTyrAspThrAlaLysGly 200

DB 541 GTGCAGGGCATCATCTACCGGGGCGCTTCTGCGGTGATGATGATCGCGCAAGCGC 600

QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTTPMetIleAlaGlnThrVal 220

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DB 661 ACGGCGGTCGCGGCGGTGTCTTACCCCTTCGACACGTCGGCGCGCAAGATGATG 720

QY 241 GlnSerGtLYaArgLysGtLYaAlaAspIleMetTyrThrGtLYaValAspCysTTPArgLys 260

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QY 261 IlePheArgAspGtLYaGtLYaLysAlaPhePheLysGtLYaAlaTTPSerAsnValLeuArg 280

DB 781 ATCTTCAGAGATGAGGGGGCAAGGCTTCTTCAAGGAGCGGTGATGCAAGCTTCGCGC 840

QY 281 GtYMetGtLYaLysAlaPheValLeuValLeuTyrAspGtLYaLysValIle 298

DB 841 GGCATGGGGGCGCTTCTGCTGTGCTGATGACGACACTCAAGAGGTGATG 894

RESULT 3
BC008935 1193 bp mRNA 11near PRI 12-JUL-2001
LOCUS
DEFINITION Homo sapiens, similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MGC:2387
IMAGE:2824067, mRNA, complete cds.
ACCESSION BC008935
VERSION BC008935.1 GI:14286273
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 1193)
Strausberg, R.
Direct Submission
Submitted (29-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA
NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgabbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMLN)
DNA Sequencing by: Institute for Systems Biology

http://www.systembiology.org
contact: amadan@systembiology.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Kettelman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9956036.
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Alignment Scores:
Pred. No.: 1.27e-144 Length: 1193
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-811-094-33 (1-298) x BC008935 (1-1193)

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QY 21 IleSerLysThrAlaValAlaProIleGtLYaArgValLysLeuLeuGlnValGlnHis 40

DB 154 ATCTCCAGACGGCGGTGCTCGGATCGAGCGGCTCAAGCTGCTGCGAGGTCCACAC 213

QY 41 AlaSerLysGlnIleAlaAlaAspLysGtLYaSerGtLYaIleValAspCysIleValArg 60

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QY 61 IleProLysGlnGlnGtLYaValLeuSerPheTTPArgGtLYaAsnLeuAlaAsnValIleArg 80

DB 274 ATCCCAAGAGAGAGGGGTGTCTCTTCTTGGAGGGGCAACCTTGCAACGTCATTCGC 333

QY 81 TTTpPheProThrGlnAlaLeuAnpPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100

DB 334 TACTTCCCACTCAAGCCCTCAACTCCGCTTCAAGGATGATGACAGAGATCTTCGCG 393

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DB 394 GGGGGCGTGGACACACACGAGTTCGAGGTACTTGGCGGCAACTGGCGCTCCGCGC 453

QY 121 GtYLaLaLaGtLYaLaThrSerLeuGysPheValTyrProLeuAspPheAlaArgThrArg 140

DB 454 GGTGGGGCGGGCGGCACTCTCTGCTTCGTTGATACCCCTTGATTTTCCAGAACCCCGC 513

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Db		694	ATGCTCCCCGACCCCAAMACACACACATCTGCTGTGACACTGTGAGATCGCGGACCTGG	753
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Db		874	ATCTTCAGAAATAGSGGGGGGCAAGGCTCTCTCAAGGGTGGCTGTCCAACGTCTCGGG	933
OY		281	GlyMetGlyGlyAlaPheValIeuValIeuTYrAspGlnIleuLYsValIle	298
Db		934	GGCATGGGGGGGCCCTTCTGCTGCTGTCTGTACGACAGCTCAAGAGAGTGAATC	987
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LOCUS			Homo sapiens solute carrier family 25 (mitochondrial carrier;	
DEFINITION			adenine nucleotide translocator), member 6, mRNA (CDNA clone	
ACCESSION			MGC:15671 IMAGE:3349670), complete cds.	
VERSION		BC007295		
KEYWORDS		BC007295.1 GI:13938330		
SOURCE		MGC:		
ORGANISM		Homo sapiens (human)		
REFERENCE		Homo sapiens		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
		1 (bases 1 to 1308)		
		Strausberg,R.L., Fellagold,E.A., Grouse,L.H., Derge,J.G.,		
		Klausner,R.D., Collins,F.S., Wagner,L., Shennem,C.M., Schuler,G.D.,		
		Altshuler,S.F., Zeeberg,B., Buettou,K.H., Schaefer,C.F., Bhat,N.K.,		
		Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,		
		Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,		
		Scapleton,M., Soares,M.B., Bonaldi,M.P., Casavant,T.L.,		
		Scheetz,T.E., Brownstein,M.J., Uedlin,T.B., Nishiyuki,S.,		
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		Armstrong,R.D., Mullahy,S.J., Bosca,S.A., McEwan,P.J.,		
		McKernan,K.C., Malek,J.A., Gunaratne,P.H., Richards,S.N.,		
		Wyllion,D.K., Wuzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,		
		Fahney,J., Helton,E., Keltman,M., Madan,A., Rodrigues,S.,		
		Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,		
		Bouffard,G.G., Blakesley,R.W., Touchman,A.J.W., Green,E.D.,		
		Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmittz,J., Myers,R.M.,		
		Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalins,D.E.,		
		Genereich,A., Schein,J.E., Jones,S.J. and Marra,M.A.		
TITLE		Generation and initial analysis of more than 15,000 full-length		
JOURNAL		human and mouse cDNA sequences		
MEDLINE		PROC. NATL. Acad. Sci. U.S.A. 99 (26), 16899-16903. (2002)		
PUBMED		2238657		
REFERENCE		12479532		
AUTHORS		2 (bases 1 to 1308)		
TITLE		Strausberg,R.		
		Direct Submission		

REMARK
COMMENT

Submitted (01-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>

Contact: MGC help desk
Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC

CDNA Library Preparation: Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada

IntOrgacc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susana Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Leticia Hsiao, Martin Krzywninski, Reba Kusche, Oliver Lee, Soo Sen Lee, Victor Ling, Carlie Mathewson, Candace Sieny, Steven Ness, Pawan Pandoh, Anna-Liisa Prabh, Pawanen Speedi, Jacqueline Schell, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stolt, Michael Thorne, Miranada Tsai, Matsja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>

Series: IVAL Plate: 22 Row: m Column: 20.

Location/Qualifiers

1. 1308

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/clone="MGC:15671 IMAG6:3349670"

/tissue_type="Eye, retinoblastoma"

/clone_lib="NIH-MGC.16"

/lab_host="DH10B-R"

/note="Vector: pOTB7"

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/gene="SLC25A6"

/note="synonyms: ANT3, ANT3Y, MGC17525"

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53. 949

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VYKTRISGIRGLXQGFSSVGGIILYAAVFGVYTAGMDLPKNTNLYVSMNTA
VYTAAGVSPEDTVARRRMMQSGRKADIMYGTVDCKRIEFDGCAAFRRGAM
NVLRMGCAFLVLYDELKVI"

278 a 399 c 390 g 241 t

BASE COUNT

ORIGIN

Alignment Scores:

Preh. No.: 1 42e-144 Length: 1308

Score: 1543.00 Matches: 298

Percent Similarity: 100.00% Conservatve: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0

DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x BC007295 (1-1308)

QY 1 MetThGluGlnAlaAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20

Db 53 ATGAGGAAAGAGCCATCTCCCTCGCCAAAGATCTTGTCGGCGAGGACATCGCGCGCC 11

QY 21 lIleSerIysThrAlaValAlaProIleGluIarValIysIleuLeuGluAlaGlnHis 40

Db 113 ATCTCCAAAGAGCGCGCTGCGCTCCATGACAGCGGAGTCAACCTGCTGCTGACGTCCAGC 17

Oy		41	AlaSerTysGlnIleAlaAlaAspLysGlnTyrIleSgLYlLeValaAspCysIleValArg	60
Db		173	GCCAGCAACGATCGCCGCCGACACAGTACAAAGGGCATCGTGAGCTCATTTGTCCG	232
Oy		61	IleProLysGlnGlnGlyValIleuSerPheTrpArgLYaSnIleuAlaAsnValIleArg	80
Db		233	ATCCCCAAGGAGCGGGCGTGCCTTCCTTGAGGGGGCAACTTGGCAACGTCATTCCG	292
Oy		81	TyrPheProThrGlnAlaIleuAsnPheAlaPheLysAspLysTyrLYsgInIlePheLeu	100
Db		293	TACTTCCCACCTCAAGCCCTCAACTTGGCTTCGCTTCACAGATTAAGTACAAGCATCTTC	352
Oy		101	GlyGlyAlaAspLysSHstThrGlnPheTrpArgTyrPheAlaGlyAsnIleuAlaSerGly	120
Db		353	GGGGGCGGTGAACAAGCACACGACAGTTGTGAAGTACTTTCGGGGCAACCTGGCTCCGG	412
Oy		121	GlyAlaIlaGlyAlaThrSerLeucCysPheValTYzProIleuAspPheAlaArgThzArg	140
Db		413	GGTCCGGCGCGGGAGACTCCCTCTGTGTTGTGTGACC GGCTGATTTCCGCAAGACCCGC	472
Oy		141	LeuAlaAlaAspValGlyLysSerGlyThzGluArgGluPheArgGlyLeuGlyAspCys	160
Db		473	CTGGCACCGGACGCTGGGAMAATCAGGCACAGACGCGAGATTCGAGGCGCTGGAGACTGC	532
Oy		161	LeuValLYslIeThrLYsSerAspGLYLleArgGlyLeuLYrgInglyPheSerValSer	180
Db		533	CTGGTAGAAGATCACCAAAGCTCCGACGGATCCGGGGCGCTGACCAAGGGCTTCAGTGTCC	592
Oy		181	ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTYzAspThrAlaLYsGly	200
Db		593	GTCGAGGGCATCATCATCTACCGGGCGGCGCTACTCGCGCTGACATACGCGCAAGGC	652
Oy		201	MetLeuProAspProLYsaSnThzHisIleValYalSerTrrPmetIleAlaGlnThzVal	220
Db		653	ATGCTCCCGCACCCCAAGAACACCCACATGCTGGTGAAGTGAATCGGCGCAACCGTGT	712
Oy		221	ThrIleValIlaGlyValIseTyrTyroPheAspThrValaArgArgMetMetet	240
Db		713	ACGGCCGTGGCGGGCGTGTCTCTACCCCTTCACACGGGCGGGCGCGCATATATATG	772
Oy		241	GlnSerGlyArgLYsGlyAlaAspIleMetTyrThzGlyThzValaAspCysTrrPArgLYs	260
Db		773	CAGTCCGGCGCCAAGGAGCGTGAATCATGTATACACGGGGCAOCTGCATGTGTGAGGAG	832
Oy		261	IlePheArgAspGlnGlyGlyLYsAlaPhePheLYsGlyAlaTrrPserAsnValIleuArg	280
Db		833	ATCTTCAGAGATGAGGGGGCGCAAGCCTTCTTCAAGGGTGTGCTGCACAGCTCTCGGG	892
Oy		281	GlyMetGlyGlyAlaPheValIleuValLeuTyrAspGluIleuLYsLYsValIle	298
Db		893	GGCATGGGGGGCGCTTCGTGCTGTCTCTGTACGACGAGCTCAAGAGAGGTGATC	946
RESULT 5				
AY007135				
LOCUS		AY007135	1344 bp	mRNA linear PRI 31-AUG-2000
DEFINITION		Homo sapiens clone CDABP0051		mRNA sequence.
ACCESSION		AY007135		
VERSION		AY007135.1		GI:9956038
KEYWORDS		FLI cDNA.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE		Anderson, B., Wentland, M.A., Ricefrante, J.Y., Liu, W. and Gibbs, R.A.		
JOURNAL		A double adaptor' method for improved shotgun library construction		
MEDLINE		Anal. Biochem. 236 (1), 107-113 (1996)		
PUBMED		96207227		
REFERENCE		2 (bases 1 to 1344)		
AUTHORS		Yu, W., Anderson, B., Worley, K.C., Muzny, D.M., Ding, Y., Liu, W.,		
		Ricefrante, J.Y., Wentland, M.A., Lennon, G. and Gibbs, R.A.		
		Large-scale concatenation cDNA sequencing		

FEATURES	source
JOURNAL	Genome Res. 7 (4), 353-358 (1997)
MEDLINE	97264341
PUBMED	9110174
REFERENCE	3 (bases 1 to 1344)
AUTHORS	Zhou,J., Yu,W., Tang,H., Mel,G., Tsang,Y.T.M., Bouck,J., Gibbs,R.A.
TITLE	Direct Submission
JOURNAL	Submitted (24-JUL-2000) Human Genome Sequencing Center and Texas Children's Cancer Center, Baylor College of Medicine, Houston, TX 77030, USA
COMMENT	The clone request should be directed to Dr. J. Margolin at Pediatrics-Hematology & Oncology, Texas Children's ERIGIN Center 102514, Houston, Texas 77030, USA. Telephone: 713-770-4583 margolinedbcm.tmc.edu.
FEATURES	location/Qualifiers
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	/note="from patient with acute lymphoblastic leukemia"
	90..986
	/note="Similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1"
	/codon_start=1
	/protein_id="AA001998.1"
	/db_xref="GI:9956039"
	/translation="MTKQATSFAPDPLAGGIAAISKTAVPPIRVKLLIOVQASAKK IAAKQKGYDTCVRIPIKEGQVLSFPMRGNLANIRITPDALNPAEDKTKQIFLG VDKTQFWRIYFAGNLASGAGATSLCFVYPLDAKRLADVSGTEREFGIGDO LTVKTSKSGINGLYOGFSVVOGIIYRAAFGYVDAGKMLPPKNTNHYISNMKIC LTKVAGVSYPEFDVVRMMQSGRGKADIMYGTVCWKRIFRDEGKAFPGAWMS NVRMGGAFAFLVYDELKRYI"
BASE COUNT	274 a 416 c 403 g 251 t
ORIGIN	
Alignment Scores:	
Pred. No.:	1.47e-144
Score:	1543.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	Gaps: 9
US-09-811-094-33 (1-298) x AY007135 (1-1344)	
QY	1 Methrctguglnalalieserphenalalysaspheleualaglyglytlealalala 20
DB	90 ATGACGGACAGGCGCATCTCTCGCCCAAAACATCTTGGCGGAGGAGCATGCGCCGCC 149
QY	21 Ileserlystpralalavalalaproillelunrgyvallylsleuleuleglvalglntls 40
DB	150 ATCTCCAAAGAGGCGCGTGGCTCCGATCCAGGCGGATCAAGCTGCTCCAGGTCCAGCAC 209
QY	41 Alaserlysglnllealalalaspysglntrlylsglyllevalaspysllevalary 60
DB	210 GCCAGCAGCAGATGCGCGCGCAGACAGACAGTACAAAGGCGATCGTGAATGCTATGTCGCC 269
QY	61 lleprrlysglunglylvalleuserphenetrrpargilyasnleualalasnvalilleary 80
DB	270 ATCCCAAGAGGAGCGGCGTGGCTGCTTCTGGAGGGGCAACCTTGCACAGTCATTCGCG 329
QY	81 Tyrphenetrrnglnalaleuasnphenalaleheysasplysttyrlysglnllephenleu 100
DB	330 TACTTCCCACTCAAGCCCTCACTCACTCCCTTCAAGGATTAAGTACAAACAATCTTCTCG 389
QY	101 glylyvalaaprylshisthrglnphetrrpargtyrphenalaglyasnleualasergly 120
DB	390 GGGGGCGTGGACAAACGACAGTCTTCGAGAGTACTTTGGGGGCAACCTGGCTCCGGCC 449
QY	121 glyalalaglyalathrserleucycysphevaltyrproleuaspphealatrghtharg 140

Db	450	GGTGGGCGCGGCGACCTCCCTCTCTCTCGTGTACCGGTGGATTTCCGCGAAGACCG	509
Oy	141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgGlnPheArgGlyLeuGlyAspCys	160
Db	510	CTGGCAGCGGAGCTGGGAAAGTCAGGCCACAGCGCGAGTTCGAGGCTGGGAGACCTGC	569
Oy	161	LeuValLysIleThrLysSerAspGlyIleArgGlyLeuThrGlnGlyPheSerValSer	180
Db	570	CTGGTGAAGATCCACCAAGTCGAGCGGCAATCCGGGGCCGTGTACCGAGGCGTTTCAGTCTCC	629
Oy	181	ValGlnGlyIleIleIleIleThrArgAlaAlaArgPheGlyValThrAspThrAlaLysGly	200
Db	630	GTGAGAGGCAATCATATCTACCGGGCGGCTACTTCGGCGGTGTACATACATACGGCCAAAGGC	689
Oy	201	MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnPheVal	220
Db	690	ATGCTCCCCGACCCCAAGACAGCAATCGTGAGTGGTACTGATGATCCGCGACACCGTG	749
Oy	221	ThrAlaValAlaGlyValValSerTyrTrpPheAspThrValAlaGargArgMetMet	240
Db	750	ACGGCCCTGGCCCGGGGTGTCTCTACCCCTTCGACAGCGTGCCGGCGGCAGTATGATG	809
Oy	241	GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys	260
Db	810	CAGTCCGGGCGCGAAGAGAGCTGACATATATACAGGGGACCGTCGACTTGGAGAGAG	869
Oy	261	IlePheArgAspGlnGlyGlyAlaAlaPhePheLysGlyAlaTrpSerAsnValLeuArg	280
Db	870	ATCTTCAGAAATGAGGGGGCGCAAGCCCTTCTTCAGGGGGGTGGTGTCAACGTCCTCGGG	929
Oy	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysValIle	298
Db	930	GGCAGTGGGGGGCGCTTCCTGTGTGTCTGTACGACGACCTCAAGAGAGTGATC	983
RESULT 6			
LOCUS	BC007850	1366 bp	mRNA
DEFINITION			Human sarpLens, similar to solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5, clone
ACCESSION	BC007850	MGCL14294	IMAGE:4136545, mRNA, complete cds.
VERSION	BC007850.1	GI:14043790	
KEYWORDS			MGC.
SOURCE			Homo sapiens (human)
ORGANISM			Homo sapiens (human)
REFERENCE			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
AUTHORS			1 (bases 1 to 1366)
TITLE			Strausberg, R.
JOURNAL			Direct Submission
COMMENT			Submitted (11-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2390, USA
REMARK			NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT			Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNI) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ http://www.nisc.mgc.nih.gov/ Contact: Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M., Benjamins, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R., Lim, M., Maduro, Q.L., Mastello, C., Mestian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Snyder, B., Stantip, S., Thomas, P.J., Tlionson, E.E., Touchman, J.W., Tsugeon, C., Vogt, J.L., Walker, M.A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/IML at: <http://image.llnl.gov>
 Series: RNAI Plate: 20 Row: 1 Column: 14
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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BASE COUNT 287 a 419 c 409 g 251 t

ORIGIN

Alignment Scores:
 Pair. NO.: 1.5e-144 Length: 1366
 Score: 1343.00 Matches: 288
 Percent Similarity: 100.008 Conservative: 0
 Best Local Similarity: 100.008 Mismatches: 0
 Query Match: 100.008 Indels: 0
 DB: 9 Gaps: 0

US-09-811-094-33 (1-298) x BC007850 (1-1366)

QY	1	Mettrhguglnalalieserphealalaysapheleuallaglylytlaaalaala	20
DB	101	ATGACGGAAAGCGCCACATCTTCGGCAAAACATTCCTGGCGAGAGCGCGCGCC	160
QY	21	lleserlystralaValaAlaProillegluarVallylsleuleuleuglnValglnHis	40
DB	161	ATCTCCAAAGAGCGCCGCGTGCATCGATCGAGGGGTGCAAGCTGCTGATGAGTCCACAC	220
QY	41	AlaserlysglnlleaalaalaspysglnlyrlysglytllaValaspCyslleValarg	60
DB	221	GCAGAGAACGATCGCCGCGCGCAAGCAGTACAAAGGCACTCTGCATCGCATTCGCGC	280
QY	61	lleprolysglunlnglyValleueserPheprarglyasnleuilaasnVallearg	80
DB	281	ATCCCAAGAGCAGCGCGCGTGCCTCTTCGTGAGGGCAACCTTCACAACTCATTCGC	340
QY	81	tyrPheprorhnglnalaleuaenphealapeulyasplystrlyrlysglnllepheleu	100
DB	341	TACTTCCCACTCAAGCCCTCACTTCGCGCTTCGAAGGATTAAGTCAAGCAGATCTTCCTG	400
QY	101	glylyValaspPysHsthrlnPheprargtyrPhealaglyasnleuilaaserly	120
DB	401	GGGGGGGTGACAAAGCAGCAGCTTCGTGAAGTCTTCGGCGCAACCTGGCGCTCGCGC	460
QY	121	glylaalaaglyalathrserleucyspheVallyrProleuasnphealargtharg	140
DB	461	GGTGGCGCGCGCGCACCTCCCTCTTCGTGTCACCGCGGTTCGCAAGAACCCGC	520
QY	141	leuallalaaspValaglylyserglythrngluarglunpheargelyleuqlaspCys	160

Db 521 CTGGCAGCGGAGCTGGGAAAGTCAAGCAGACGCGGAGTCCGAGCGCTGGGAGACTGC 580
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Db 581 CTGTGAAGATCACCAAGTCCGACGCGATCCGGGGCTGTGACCAAGGCGCTTCACTGTCTCC 640
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QY 201 MetLeuProAspProIysAsnThrHisIleValIleSerIlePheIleIleIleIleIleIleIle 220
Db 701 ATCTCCCGGACCCCAAGAACGCGATCTGTGTGATGATGATGATGATGATGATGATGATGATG 760
QY 221 ThrAlaValAlaGlyValValIleSerIleThrProPheAspThrValArgArgArgMetMet 240
Db 761 ACAGCGCGTGGCGCGGCGGTCTTACCTTGCACACGCGTGGCGGCGGCGCATGATGATGATG 820
QY 241 GlnSerGlyArgGlySerGlyAlaAspIleMetIleIleIleIleIleIleIleIleIleIleIle 260
Db 821 CAGTCCGGGCGCAAGAGAGCTGACATCATGTACACGCGGCGGCGGCGGCGGCGGCGGCGG 880
QY 261 IlePheArgAspGlnGlyIleGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIle 280
Db 881 ATCTTCAGAGATAGAGGGGCGGACAGGCTTCTTCAAGGGTCTGTGTCTCAAGGCTGTCTGG 940
QY 281 GlyMetGlyGlyAlaPheValIleuValIleuTyraSpGluLeuIysIysValIle 298
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RESULT 7
BC031912
LOCUS 1399 bp mRNA linear PRI 26-JUN-2002
DEFINITION Homo sapiens, solute carrier family 25 (mitochondrial carrier);
adenine nucleotide translocator, member 6, clone MGC:29984
IMAGE:5141625, mRNA, complete cds.
ACCESSION BC031912
VERSION BC031912.1 GI:21594692
KEYWORDS MGC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1399)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: gcrabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amebcm.tmc.edu
Gonathone, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAC Plate: 42 Row: P Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Similarity but not
identity to protein.
FEATURES
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TVTAAGVVSYPEDTVRRMMQSGRRADIMYTGTVDCWKIFRDEGGKAFKAGAMS
NVLRCMGAFVLVLYDELKKVI"
BASE COUNT 300 a 419 c 414 g 266 t
ORIGIN
Alignment Scores:
Pred. No.: 1.55e-144 Length: 1399
Score: 1543.00 Matches: 298
Percent Similarity: 100.008 Conservative: 0
Best local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
Gaps: 0
US-09-811-094-33 (1-298) x BC031912 (1-1399)
QY 1 MetThrGlnIleAlaIleSerPheAlaIleAspPheLeuAlaGlyIleIleAlaAla 20
Db 38 ATGACGAAACAGGCGATCTCTTCCGCAAGACTTCTGTGCGAGGACATCGCGCGCC 97
QY 21 IleSerIleThrAlaValAlaProIleGluArgValIleLeuLeuGlnIleGlnHis 40
Db 98 ATCTCCAGACGCGCGGTGCTCGATGACGCGGTCTCAAGTCTGCTCGAGTCCAGAC 157
QY 41 AlasSerIleGlnIleAlaAlaAspIleGlnIleIleValIleValIleValIle 60
Db 158 GCCAGCAAGAGATCGCGCGCGCAAGCAGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 217
QY 61 IleProIleGlnIleGlnIleValIleSerPheIleIleValIleValIleValIle 80
Db 218 ATCCCAAGAGGAGGCGGTGCTCTGTGAGGGGCAACCTTGCCACGTCATTCGCG 277
QY 81 TyrPheProThrGlnAlaIleuAsnPheAlaPheIleAspIleIleIleIleIleIle 100
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OY	281	GlyMetGlyLYsAlaPheValLeuValLeuTyrAspGlnLeuLYsValIle	298
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LOCUS	1466 bp	mRNA	linear	PI-12-JUL-2001
DEFINITION	BC008737	Home sapiens, similar to solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, clone MCC:3042722, IMAGE:3342722, mRNA, complete cds.		

ACCESSION	BC008737
VERSION	BC008737.1
KEYWORDS	GI:14250566
SOURCE	MGC
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 1466)
Strausberg, R.
Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian
Genetics Office, National Cancer

REMARK	COMMENT
NIH-MGC project URL: http://mgc.ncl.nih.gov	Contact: MGC help desk

Direct Submission
 Submitted (25-MAY-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-rt@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILINT)
 DNA Sequencing by: National Institutes of Health Intramural
 Gaithersburg Center (NISC),
 Gaithersburg, Maryland
 Web site: <http://www.nisc.nih.gov/nisc.mgcenbgr1.nih.gov>
 Contact: nisc.mgcenbgr1.nih.gov
 Shencherin, B., Wetherby, R.D., Beckstrom-Sternberg, S.M.,
 Benjamin, B., Yakselesky, R.M., Bouffard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, R.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Mastaglio, C., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Snyder, B., Stanlidop, S., Thomas, P.J.,
 Tlousone, E.E., Touchman, D.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H. and Green, E.D.

Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/ILN at: <http://image.lln.gov>
 Series: IRRL Plate: 5 Row: 0 Column: 23
 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis.

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QY      101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
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QY      121 GlyAlaAlaGlyAlaIleSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
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DEFINITION Sequence 2 from Patent WO0132876.
ACCESSION AX134719
VERSION   AX134719.1 GI:14271236
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SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
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           Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS   Murphy,A.N., Clevenger,W., Wiley,S.E., Andreyev,A.Y., Frigieri,L.G.,
           Velicelbeli,G. and Davis,R.E.
TITLE      Compositions and methods for determining interactions of
           mitochondrial components, and for identifying agents that alter
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           Patent: WO 0132876-A 2 10-MAY-2001;
           MITOKOR (US)
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      181 ATTCGAAGAGAGAGAGAGATTTGCTCTTCTTGGCGCGGTAACTGGCAATGTCATCAGA 240
QY      81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
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QY      101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
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ACCESSION AX301847.1 GI:17382904
VERSION
KEYWORDS
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
AUTHORS Anderson, C.M., Davis, R.E., Clevenger, W., Willey, S.E., Miller, S.W., Szabo, T.R., Ghosh, S.S., Moos, W.H., Pal, Y. and Carroll, A.K.
TITLE Production of adenine nucleotide translocator (ant), novel ant ligands and screening assays therefor
JOURNAL Patent: WO 0185944-A 2 15-NOV-2001;
MITOKOR (US)
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BASE COUNT 209 a 223 c 246 g 219 t
ORIGIN

Alignment Scores:
Pred. No.: 6.87e-136 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0

US-09-811-094-33 (1-298) x AX301847 (1-897)

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QY 281 GlyMetGlyGlyAlaPheValIleuValLeuTyArgAspGluLeuLys 296
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RESULT 14
LOCUS HUMATPC 1228 bp mRNA linear PRI 27-APR-1993
DEFINITION Human ADP/ATP carrier protein mRNA, complete cds.
ACCESSION J02683
VERSION J02683.1 GI:179246
KEYWORDS ADP/ATP carrier protein.
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE
1 (bases 1 to 1228)

AUTHORS Battini, R., Ferrari, S., Kaczmarek, L., Calabretta, B., Chen, S.T. and Basegga, R.

TITLE Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated

JOURNAL MEDLINE J. Biol. Chem. 262 (9), 4355-4359 (1987)

PUBMED 8716606

COMMENT 3031073

Original source text: Human SV40 transformed fibroblast, cDNA to mRNA, clone hp2F1.

Draft entry and computer-readable sequence for [1] kindly provided by R. Battini, 09-MAR-1987.

The steady state levels of the ADP/ATP carrier mRNA are growth-regulated. They increase when quiescent cells are stimulated by serum, platelet-derived growth factor (PDGF), or epidermal growth factor (EGF), but not by platelet-poor plasma or insulin. mRNA levels of the ADP/ATP carrier decrease when growing HL-60 cells are induced to differentiate by either phorbol esters or retinoic acid.

FEATURES

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ORIGIN Unreported.

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Percent Similarity: 96.96% **Conservative:** 13

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US-09-811-094-33 (1-298) x HUMATPC (1-1228)

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DB 70 ATGCACAGATGCCGCGCATTCCTGCCAAGAGACTTCCTGCGAGTGGCCGACGCC 129

QY 21 IleSerIleThrAlaValAlaProIleGluArgValIleuLeuLeuGlnHis 40

DB 130 ATCTCCAAAGACGGCGGTAGCGCCATCGACGGGCTGAAGCTGCTGCGAGGTCACAT 189

QY 41 AlaSerIleGlnIleAlaAlaAspIleGlnIleValIleAlaIleValArg 60

DB 190 GCGAGCAAGCAGATCTACGAGATTAAGCAATACAAAGCCTTTATAGACTCGGGTCCGT 249

QY 61 IleProIleGluGlnIleValIleuSerPheTrpArgGlyIleuLeuAlaValIleArg 80

DB 250 ATTCCTCCAAAGACGGCGGTAGCGCCATTCCTGCGAGGTCACATCGATCAGCA 309

QY 81 TyrPheProThrGlnAlaLeuAspPheAlaPheIleAspIleValIlePheLeu 100

DB 310 TACTTCCCAACCCAGGCTCTTAACCTCGCTCAAGATTAACAAAGCATCTTCCTG 369

QY 101 GlyIleValAspIleHisIleThrGlnPheTrpArgIlePheAlaGlyIleuLeuAlaSerGly 120

DB 370 GCGGCGTGGACAGAGAACCCAGTTTGGCGCTACTTCTCAGGGAATCGGCATCGGGT 429

QY 121 GlyAlaAlaGlyAlaThrSerIleuCysPheValIleTyrProLeuAspPheAlaArgThrArg 140

DB 430 GGTGCGGAGGGGCCACATCCCTGCTTTGGTATACCTCTGATTTGCGGTACCGGT 489

QY 141 LeuAlaAlaAspValGlyIleSerGlyThrGluArgGluPheArgGlyIleuGlyAspCys 160

DB 490 CTACGAGCTGATGTGGTAAAGCTGAGCTGAAGGAAATCCGAGCCCTGGTACTGC 549

QY 161 LeuValIleIleThrIleSerAspGlyIleArgGlyLeuTyrGlnIlePheSerValSer 180

DB 550 CTGGTTAAGATCTACAAATCTGATGGATTAAGGCGCTGTACCAAGCTTTAACGTCT 609

QY 181 ValGlnGlyIleIleIleThrArgAlaAlaIleTyrPheGlyValIleTyrAspThrAlaVal 200

DB 610 GTGCAGGATATATCTATCTACACAGCGGCTACTTGGTATCTATGACACTGCAGAAAGGA 669

QY 201 MetLeuProAspProIleAsnThrHisIleValIleValSerTrpMetIleAlaGlnThrVal 220

DB 670 ATGCTTCGGATCCAGAACACTCATCTGATATGAGCTGGATGATGCGACGACTGTC 729

QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgIleMetMet 240

DB 730 ACTGCTGTGCGCGGTGACTTCTCATTCATTTGACACCGCTTCGCGCGCATGATGATG 789

QY 241 GlnSerGlyArgIleGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgIle 260

DB 790 CAGTCAAGGCGGCAAGGAAGACTGACATCATGTATACACAGGCGCTTGACTGCTGGCGAAG 849

QY 261 IlePheArgAspGluGlyIleGlyIleValIlePhePheGlyValAlaTrpSerAsnValLeuArg 280

DB 850 ATTCGCTGATATAGAGAGGCAAGCTTTTTCAGGGGTCAAGTGCATGTTCTCAGA 909

QY 281 GlyMetGlyGlyAlaPheValLeuValIleuTyrAspGluLeuIleuLysIle 296

DB 910 GGCATGGGCGCTTTTGTGCTTGTGCTTGTATGATGAATCAAGAAG 957

RESULT 15

AB065433

LOCUS Bos taurus mRNA for adenine nucleotide translocator 2, complete

DEFINITION

ACCESSION AB065433

VERSION AB065433.1 GI:18642495

KEYWORDS

SOURCE Bos taurus (cow)

ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

REFERENCE

AUTHORS Yamazaki, N., Shinohara, Y., Tanida, K. and Terada, H.

TITLE Structural properties of mammalian mitochondrial ADP/ATP carriers: identification of possible amino acids that determine functional differences in its isoforms

JOURNAL Mitochondrion 1, 371-379 (2002)

AUTHORS Yamazaki, N., Shinohara, Y. and Tanida, K.

TITLE Direct Submission.

JOURNAL Submitted (11-JUL-2001) Naoshi Yamazaki, University of Tokushima, Faculty of Pharmaceutical Sciences, Stomach, Tokushima, Tokushima 770-8505, Japan (E-mail: yamazaki@fc.ph.tokushima-u.ac.jp, Tel: 81-88-653-7279)

FEATURES

source

CDS

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Thu Aug 28 08:34:55 2003

us-09-811-094-33.p2n.rge

Page 14

1121 1136
NLRLMGGAFFVLVLYDEIKRET"

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BASE COUNT	283 a	275 c	291 g
ORIGIN			297 t

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US-09-811-094-33 (1-298) x AB065433 (1-1146)

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QY	21	IleSerLystrIleAlaValAlaProIleGluArgValIleLeuIleLeuGlnValGlnHis	40
Db	64	ATCTCAAGACCGACGCTGGCCCATCGAGGGGTAAAGCTCTCTCGACGGTGCAGAT	123
QY	41	AlaSerLystrGlnIleAlaIaAspLystrGlnIleValIleAlaPcysIleValArg	60
Db	124	GGCAGACAGCCAAATCACTCGATTAAGCAGTACAAAGGGCATATATGACTGGGGTGTCT	183
QY	61	IlePcLystrGlnGlnIleValIleuSerPheTrpArgIleValIleAlaIleValIleArg	80
Db	184	ATCCCAAGAGGACAGGGAGTCTGTCTTCTGGCGGTGGTAACTGGCCATATGATATA	243
QY	81	TyrPheProThrGlnAlaIleuAsnPheAlaPheIleAspLystrIleGlnIlePheLeu	100
Db	244	TACTTCCCAACCCAGGCTCTCAACTTCCTCTTCACAAATATTAATACAAACAAATCTTCG	303
QY	101	GlyGlyValaIleAspLystrHisIleThrGlnPheTrpArgIlePheAlaIleAlaIleSerGly	120
Db	304	GGGGGTGTGGCAAGAGACCGACAGTTCCTGGCGCTACTTCACAGGCAATCTGGCATCAGGT	363
QY	121	GlyAlaIleAlaIleAspSerLeuGlyPheValIleProIleuAspPheAlaIleArgThrArg	140
Db	364	GGGTGGCCGGGGCCACTTCCCTGTGTGTTCGGTACCCCTCTCGACTTCGGCCGTAACCCGT	423
QY	141	LeuAlaIleAspValGlyLystrSerGlyTrpGluArgGluPheArgGlyLeuGlyIleAspCys	160
Db	424	CTAGCAGCCGAGGTGGCAAAAGCTGAGCTGAAGGAAATTCAGAGGCTCGGTGGTACTGT	483
QY	161	LeuValLystrIleThrLystrSerAspGlyIleArgGlyLeuTrpGlnIlePheSerValSer	180
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QY	181	ValGlnGlyIleIleIleTyrArgAlaAlaIleTyrPheGlyValIleTyrAspThrAlaIleGly	200
Db	544	GTCAGAGGATTATATCTACCCAGCTGGCTCACTTCGGTATCATATACACTGCCCAAGGA	603
QY	201	MetIleProAspProLystrAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal	220
Db	604	ATGTTCTTCAGAACTCCCAAAACACTCATATCTTCAACCACTGGATGATGCCAATACATCAGT	663
QY	221	ThrAlaValAlaGlyValaIleSerTyrProPheAspThrValAlaArgArgMetMetMet	240
Db	664	ACGGCAATGTCCGGGTGACTCTCTATCACTTTCAGACTGTGGCTCGCCGCAATGATG	723
QY	241	GlnSerGlyIleArgLystrGlyValaIleAspIleMetTyrThrGlyThrValAspCysTrpArgLystr	260
Db	724	CAGTCAGAGGGCCAAAGAACTCATATCATGTGTACACAGGACAGCTGTCTGTCTGGAGAG	783
QY	261	IlePheArgAspGluGlyGlyValaIlePheIleGlyGlyIleTyrPheSerAsnValleuArg	280
Db	784	ATTCTCTGTATCAGAAAGAGCCAAAGCCTTTTTCAAAGCGGTGTGTCTCATATGTCTCAGA	843

Qy	281	GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys	296
		:	
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Search completed: August 27, 2003, 13:44:04
Job time : 4150 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 27, 2003, 05:30:34 ; Search time 334 Seconds

(without alignments)
2408.481 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEQAIISFAKDLAAGIAA.....LNGMGAFVLYLDELKVI 298

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	1543	100.0	897	21	AAD00521	Human adenine nucl
2	1543	100.0	897	22	AA505903	Human adenine nucl
3	1543	100.0	897	22	AA516690	DNA encoding human
4	1543	100.0	1212	22	AA158797	Human polynucleoti
5	1543	100.0	2035	22	AA160583	Human polynucleoti
6	1510	97.9	2592	25	ABX63152	Human cDNA #152 d1
7	1463	94.8	1225	24	AA148635	Human insulin rece
8	1454	94.2	897	21	AAD00520	Human adenine nucl
9	1454	94.2	897	22	AA505902	Human adenine nucl
10	1454	94.2	897	22	AA516689	DNA encoding human
11	1424	92.3	1196	24	ABX63420	Rat sequence diffe
12	1418	91.9	2213	25	ACC46652	Human dltlp organe
13	1417	91.8	1156	23	AA591243	DNA encoding novel
14	1412	91.5	1177	19	AAV36479	Anti cDNA. Mus sp
15	1405	91.1	1259	19	AAV36480	Anti cDNA. Mus sp
16	1385.5	89.8	894	21	AAD00519	Human adenine nucl
17	1385.5	89.8	894	22	AA505901	Human adenine nucl
18	1385.5	89.8	894	24	AA516688	DNA encoding human
19	1385.5	89.8	1024	25	ABX83302	Toxicologically re
20	1385.5	89.8	1320	24	ABX65029	Invertebrate forag
21	1356.5	87.9	1116	24	ABX83761	Human cDNA diffe
22	1356.5	87.9	1116	24	ABN95598	Gene #2096 used to
23	1356.5	87.9	1116	24	ABX69347	Prostate cancer re
24	1294.5	81.3	1581	23	ABL18531	Drosophila melanog
25	1254.5	81.3	1750	23	ABL20967	Drosophila melanog
26	1193	77.3	2706	22	AA529836	Human cytoskeletal
27	1193	77.3	2706	22	AA535083	DNA #33 encoding h
28	1193	77.3	220895	24	ABX64798	Human cDNA diffe
29	1167	75.6	5407	23	ABL18530	Drosophila melanog
30	1167	75.6	8031	23	ABL20966	Drosophila melanog
31	1165.5	75.5	1251	23	AA579610	DNA encoding novel
32	1137.5	73.7	1033	23	ABX03127	Drosophila melanog
33	1119	72.5	1781	24	AD333664	Human TRICH-19 cDN
34	1119	72.5	1803	23	ABX71399	Human metabolism-a
35	1099	71.2	4545	23	AA568190	DNA encoding novel
36	1081	70.1	687	24	ABQ56282	Human ovarian anti
37	1043.5	67.6	3406	23	ABL03126	Drosophila melanog
38	981	63.5	669	24	ABX3737	Human TRICH encod
39	979.5	63.5	5768	24	ABL61797	Colon adenocarcino
40	936	60.7	720	24	ABX76857	Frog embryonic gen
41	936	60.7	720	24	ABX76969	Frog embryonic gen
42	840	54.4	639	24	ABX709322	Phase-1 Rat C7 gen
43	802	52.0	707	21	AAA01634	Human colon cancer
44	796	51.6	943	24	ABX74319	Bovine embryonic g
45	788.5	51.1	906	24	ABX31907	Candida albicans e

ALIGNMENTS

RESULT 1
AAD00521
AAD00521 standard; cDNA: 897 BP.
ID
XX
AC AAD00521;
XX
DT 29-AUG-2000 (first entry)
XX
DE Human adenine nucleotide translocator ANT3 cDNA.
XX
KW Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurologic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antipsoriatic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;

PN W0200132876-A2.
 XX 10-MAY-2001.
 XX 03-NOV-2000; 2000MO-US30535.
 XX 03-NOV-1999; 99US-0434354.
 XX (MITO-) MITOKOR.
 PA Murphy AN, Clevenger W, Wiley SE, Andrejev AV, Fritzer LG;
 PI Vellecebeli G, Davis RE;
 XX P-PSDB: AA001200.
 DR WPI: 2001-291054/30.
 XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 PS Disclosure: Fig 1; 186pp; English.

CC The present sequence encodes for human adenine nucleotide translocator-3
 CC (ANT3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunction of cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

SO Sequence 897 BP; 174 A; 274 C; 287 G; 162 T; 0 other;

Alignment Scores:

Pred. No.: 1.62e-172 Length: 897
 Score: 1543.00 Matches: 298
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 22 Gaps: 0

US-09-811-094-33 (1-298) x AAS05903 (1-897)

QY 1 MetThGlnGlnAlaIleSerPheAlaLysASPheLeuAlaGlyIleAlaIaIa 20
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 QY 11leSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValHis 40
 DB 61 ATCTCCAAAGACGGCGCTGGCTCCGATCGACGGGTCGAAGTGTGCTGCGACGAC 120
 QY 41AlaSerLysGlnIleAlaIaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 DB 121 GCGAGCAAGCAAGTCCCGCCGCAAGCAAGTCTGCACTGATTCGCGC 180
 QY 61IleProLysGlnGlnIleValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
 DB 181 ATCCCAAGAGGAGCGGCTGCTCTCTGAGAGGGCAACCTTCGCAACGTCATTCGC 240
 QY 81TyrPheProThrGlnIleAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100

DB 241 TACTCCCACTCAACCCCTCAACTTCGCCCTTCACAGATTAAGTACAGCAGATCTTCCTG 300
 QY 101 GlyIValAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 DB 301 GGGGGGTGGACAGACACAGCGATCTTGAGGTACTTTCGGGCAACTGGCTCCGGC 360
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 DB 361 GGTGGCGCGCGCGACCTCCCTGCTTCGTCTGATCCCGGTGATTTTGGACAAACCCGG 420
 QY 141 LeuAlaAlaAspValAlaLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 DB 421 CTGGCAGCGGACGTGGGAAAGTCAAGCAGACCGGAGTTCGAGGCGCTGGAGACTGC 480
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 DB 481 CTGGTGAAGATCAACAGTCCGACGCGGCTTCGACCAAGGCTTCACTGCTCC 540
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 DB 541 GTCCAGGGCATCATCATCTACCGGGCGCTACTTGGCGTGTACGATACGGCCAAAGGC 600
 QY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerTrpMetIleAlaGlnThrVal 220
 DB 601 ATGCTCCCGACCCCAAGACAGCACATCTGTGTAGTGAATGATCGGACAGCCGTG 660
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgArgMetMet 240
 DB 661 ACGGCGGTGGCGCGGTGTCTCTACCTTGACACAGGTGGCGGCGCATGATGATG 720
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrParGlys 260
 DB 721 CAGTCCGGGGCAAGAGAGCTGACATCATGTACACGGGCACTGCTGTGAGAGAG 780
 QY 261 IlePheArgAspLysGlnGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 DB 781 ATCTTCAAGATAGAGGGGCAAGGCTTCTTCAAGGCTGCTGCTCCAAAGCTTCGCGG 840
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
 DB 841 GGCATGGGGGCGCTTCTGCTGCTGTCTGTACGACAGCTCAAGAAAGTGATC 894

RESULT 3
 AAS16690 standard; cDNA; 897 BP.
 ID AAS16690:
 AC AAS16690:
 DT 14-FEB-2002 (first entry)
 DE DNA encoding human adenine nucleotide translocator 3 (ANT3).
 XX Human: adenine nucleotide translocator; ANT; ss;
 KW mitochondrial matrix protein.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..897
 FT /tag= a
 FT /product= "Adenine nucleotide translocator 3 (ANT3)"
 PN W0200185944-A2.
 PD 15-NOV-2001.
 XX 11-MAY-2001; 2001MO-US15416.
 XX 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;

Pred. No.: 5,37e-162 Length: 897
 Score: 1454.00 Matches: 274
 Percent Similarity: 96.96% Conservative: 13
 Best Local Similarity: 92.57% Mismatches: 9
 Query Match: 94.23% Indels: 0
 DB: 21 Gaps: 0

US-09-811-094-33 (1-298) x AAD00520 (1-897)

QY 1 MethThrglUGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 Db 1 ATGACAGATGCCGATGTCCTTCGCCCAAGGACTTCTTGGCAGGTGAGTGGCCGACGCC 60
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnAla 40
 Db 61 ATCTCCAGACGGCGGTAGCGCCCATCGAGCGGGTCAAGCTGCTGTGACGGTGCAGCAT 120
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 Db 121 GCCAGCACGACGACTGCTGAGTAAACATACAAAGGCAATATAGACTGCGTGCCTCGT 180
 QY 61 IleProLysGluGlnGlyValLeuSerPheTyrPArgGlyAsnLeuAlaAsnValIleArg 80
 Db 181 ATTCACAGGACGAGGAATCTGCTCTTCTGCGCGGTACCTGGCCCAATGTCATCAGA 240
 QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 241 TACTCCACACCGAGCTCTTAACTCGGCTTCAAAAGATAAATACAAAGCAGATCTCCTG 300
 QY 101 GlyGlyValAspLysIleThrGlnPheTyrPArgTyrPheAlaGlnLysLeuAlaSerGly 120
 Db 301 GGTGTGTGTGACAAAGAAACCCAGTTTGGCGCTACTTTCAGAGGATCTGGCATCGGCT 360
 QY 121 GlyAlaAlaGlyValaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 361 GGTGGCGGAGGGGCCACATCCCTGTTTGTGTACCTCTTATTTTGGCCGTACCCGT 420
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 421 CTAGCAGCTGATGTGGTAAAGCTGAGGTGAAAGGAATTCGAGGCGCTGCTGACTGC 480
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 481 CTGGTTAAATCTACAAATCTGATGGATTAAGGCGCTGTACCAAGGCTTTAACTGCTCT 540
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 541 GTCCAGGATATATCATCTACAGCGCGCTACTTGGTATCTATGACACTGCAAGAGGA 600
 QY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerTyrMetIleAlaGlnThrVal 220
 Db 601 ATGCTTCGCGATCCCAAGAACACTCATCTGATCAGCGGATGATCGACAGACTGTC 660
 QY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgArgMetMetMet 240
 Db 661 ACAGCTGTGGCCGGGTGACTCTTATCCATTTGAAACCGTTGCGCGCCGATGATGATG 700
 QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyIleValAspCysTyrPArgLys 260
 Db 721 CAGTACGGCGGCAAAAGAACTGACATCATCTACACAGGACCGTTGATCTCTGCGGAG 780
 QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTyrPheSerAsnValLeuArg 280
 Db 781 ATGCTCTGTGATGAAAGAGCAAAAGCTTTTTCAAAGGTCATGATGATGATGATGATG 840
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
 Db 841 GGCATGGGTGGTCTTTGTGTGTGTATGATGAAATCAAGAG 888

RESULT 9
 AAS05902
 ID AAS05902 standard; cDNA; 897 BP.
 XX

AC AAS05902;
 XX 07-SEP-2001 (first entry)
 DT Human adenine nucleotide translocator-2 (ANT-2) cDNA sequence.
 XX
 XX Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 1..897
 FT /tag- a
 FT /product- "ANT-2"
 XX
 PN W0200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000MO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelel G, Davis RE;
 DR P-PSDB; AAU01199.
 XX
 XX WPI; 2001-291054/30.
 DR
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 1; 186pp; English.
 XX
 CC The present sequence encodes for human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g., cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g., ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g., green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g., cancer, and deafness.
 XX
 SQ Sequence 897 BP; 209 A; 223 C; 246 G; 219 T; 0 other;

Alignment Scores:

Pred. No.: 5,37e-162 Length: 897
 Score: 1454.00 Matches: 274
 Percent Similarity: 96.96% Conservative: 13
 Best Local Similarity: 92.57% Mismatches: 9
 Query Match: 94.23% Indels: 0
 DB: 22 Gaps: 0

US-09-811-094-33 (1-298) x AAS05902 (1-897)

DB 101 ATCCCAAGAGCAGGAAAGTTCTGTCCTTGGCCCGGTACCTGGCCCAAGTCAATCAAGA 240
 QY 81 TyrPheProthrglnAlaLeuAnpHeaLapheLysAspLysTyrLysGlnIlePheLeu 100
 DB 241 TACTTCCCAACCCAGGCTTAACTGGCTTCAAAAGTAATATACAGAGATCTTCTCG 300
 QY 101 GilyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 DB 301 GGTGGTGTGACAGAGAAACCCAGTTTGGCGCTACTTGTGACAGGAATCTGGCATCGGGGT 360
 QY 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
 DB 361 GGTGCGGAGGGGGCCACATCCCTGTGTTTGTATACCCCTTGATTTTGGCCGTAACCGGT 420
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 DB 421 CTAGACAGTGAATGTGGTAAAGCTGAGCTGAAAGGAATTCAGAGGCTCGTGAATGCTC 480
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 DB 481 CTGGTTAAGATCTACAAATCTGATGGATTAAGGGCGGTACCAAGGCTTTAACTGTCT 540
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 DB 541 GTGCGGGTATATATCTACCGAGCCGCTACTGCTGGTATATGACACTGCAAGAGGA 600
 QY 201 MetLeuProAspProLysAsnThrHisIleValLysTyrPheTyrMetIleAlaGlnThrVal 220
 DB 601 ATGCTCCGATCCCAAGACACTCACAATCGTCATGATGATGATGATGATGATGATGATG 660
 QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
 DB 661 ACTGCTGTGGCGGGGTGTGACTTCTCATCTTGTACACCGTTCGCGCGCATGATGATG 720
 QY 241 GlnSerGlyArgLysGlyAlaLysPheMetTyrThrGlyThrValAspCysTrpArgLys 260
 DB 721 CAGTACAGGCGCCAAAGAGACACTGATCATGACAGACAGCCTTGACTGCGGGAAG 780
 QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
 DB 781 ATTCGTCGATGAAGAGAGGAGCAAGCTTTTTCAGAGGGTGCATGTCATGTTCTCAGA 840
 QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysLys 296
 DB 841 GGCATGGGTGGTCTTGTCTTGTCTGTATGATGAATCAAGAGAAG 888
 RESULT 11
 ABR63420
 ID ABR63420 standard; cDNA; 1196 BP.
 AC ABR63420;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1327.
 XX
 KW Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 XX differential expression; centrilobular necrosis; steatosis.
 OS Rattus norvegicus.
 XX
 PN WO200210453-A2.
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US23872.
 XX
 PR 31-JUL-2000; 2000US-222040P.
 PR 02-NOV-2000; 2000US-244880P.
 PR 11-MAY-2001; 2001US-290029P.
 PR 15-MAY-2001; 2001US-290645P.
 PR 22-MAY-2001; 2001US-292336P.
 PR 06-JUN-2001; 2001US-293798P.

PR 13-JUN-2001; 2001US-297457P.
 PR 19-JUN-2001; 2001US-298884P.
 PR 09-JUL-2001; 2001US-303459P.
 XX
 PA (GENE-) GENE LOGIC INC.
 XX
 PI Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 DR WPI: 2002-241625/29.
 XX
 PT Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or
 PT cells exposed to the toxin and comparing these to gene expression in
 PT unexposed tissues or cells -
 PS
 XX
 PS Claim 1; Seq ID No 1327; 239pp; English.
 CC
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic
 CC effect of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression.
 CC The method can also be used to identify an agent which modulates the
 CC toxic response and predict cellular pathways that a compound modulates
 CC in a cell. The methods utilise a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity
 CC is characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent.
 XX
 XX Sequence 1196 BP; 295 A; 279 C; 326 G; 296 T; 0 other;
 SQ
 Alignment Scores:
 Pred. No.: 2, 83e-158 Length: 1196
 Score: 1424.00 Matches: 267
 Percent Similarity: 95.648 Conservative: 18
 Best Local Similarity: 89.608 Mismatches: 13
 Query Match: 92.298 Indels: 0
 DB: 24 Gaps: 0
 US-09-811-094-33 (1-298) x ABR63420 (1-1196)
 QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyLysIleAlaAlaAla 20
 DB 76 ATGGGGGATCAGGCTTTGAGCTTCTTAAAGACTTCTGCGAGGTGATCGCGCGCGC 135
 QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnHis 40
 DB 136 GTCTCCAAAGCCGGGTGCGCCCGATCGAGAGGGTCAAACTGCTGTCAGATCCAGCAT 195
 QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAlaPcysIleValArg 60
 DB 196 GCGAGCAACACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 255
 QY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80

DB 256 ATCCCGAGAGAGCGGCTTTCTCTCCCTTCGAGAGGGCTTACCTGGCCAGCTGATCCGG 315
 QY 81 TyrPheProThrGlnAlaLeuAspPheAlaPheLeuAspLysPheLysLysLeuPheLeu 100
 DB 316 TACTTCCCGACCGACCAAGCTCTCACTTCCCTTCAAGACACAAGATACAGAGATCTCCCG 375
 QY 101 GlyGlyValAspLysHisThrGlnPheThrPheArgPheAlaGlyAsnLeuAspLysGly 120
 DB 376 GAGAGTGGAGTCTCTAAGACATTCGGCGCTTACTGCTGCTGCTGCTGCTGCTGCTGCT 435
 QY 121 GlyAlaAlaGlyAlaPheSerLeuPheValTyrPheLeuAspPheAlaThrArg 140
 DB 436 GGGGCGAGCTGGGCTTACCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 495
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspLys 160
 DB 496 CTGGCTGGCGAGCTGGGCAAGGATCTTCCAGCGCTGATTCATGAGGCGTGGTGTGCTGT 555
 QY 161 LeuValLysIleThrLysSerAspGlyLeuArgGlyLeuTyrGlnGlyPheSerValSer 180
 DB 556 CTACACCAAGATCTCAAGTCTGATGGCTGAGAGGCTCTTACAGAGGCTTCACTGCTCT 615
 QY 181 ValGlnGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 200
 DB 616 GTGCGAGGCTACATCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 675
 QY 201 MetLeuProAspProLysAsnThrHisIleValIleSerThrMetIleAlaGlnThrVal 220
 DB 676 ATGCTGCTCGAGCCCGACCAAGATGTCACATTTATGTGACCTGATGCTGCGACAGTGTG 735
 QY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgMetMetMet 240
 DB 736 ACAGCGGAGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 795
 QY 241 GlnSerGlyValGlyGlyAlaAspIleMetTyrThrGlnValAlaAspLysPheArgLys 260
 DB 796 CAGCTGCGCGAGAGGCGCTGATTTATGTGACAGCGGAGCGTGTGCTGCTGCTGCTGCT 855
 QY 261 IlePheArgAspGlnGlyGlyAlaPhePheLysGlyAlaTyrPheAsnValIleArg 280
 DB 856 ATTCGCAAAAGATGAGAGAGCGCAAGCTTCTTCAAAAGGCGTGTGCTGCTGCTGCTGCT 915
 QY 281 GlyMetGlyGlyAlaPheValLeuTyrAspGlnLeuLysValIle 298
 DB 916 GGCATGGGCGCTCTTCTGATTTGCTATGATGATGATGATGATGATGATGATGATGATG 969
 RESULT 12
 ACC46652
 ID ACC46652 standard; cDNA; 2213 BP.
 NC ACC46652;
 AC 02-JUN-2003 (first entry)
 DE Human dithp organelle-associated protein-encoding cDNA.
 XX Human; dithp: diagnostic and therapeutic polynucleotide; diagnosis;
 XX cancer; cell proliferative disorder; autoimmune disorder;
 XX inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 XX neurological disorder; gastrointestinal disorder; transport disorder;
 XX connective tissue disorder; drug screening; proteome analysis;
 XX gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 XX disease model; toxicological testing; transcript imaging;
 XX organelle-associated protein; gene; ss.
 OS Homo sapiens.
 XX
 XX WO200297031-A2.
 PN 05-DEC-2002.
 PD 27-MAR-2002; 2002W0-US10056.
 XX
 PF

XX 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299775P.
 PR 20-JUN-2001; 2001US-300001P.
 XX
 PA (INCYTE GENOMICS INC.
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gletzen D, Chinn J.
 PI Daffo GE, Hillman JL, Yu YF, Tuason O, Yap PE, Amato SR,
 PI Daugherty SC, Dan TC, Liu TF, Nguyen DA, Kleefeld T, Gertlin EH,
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SK, Harris B,
 PI Flores V, Marwaha R, Lo A, Lan RT, Urashka ME;
 XX
 DR WPI; 2003-129518/12.
 DR P-PSDB; ABR41715.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for
 PT identifying test compound which specifically binds to a polypeptide
 PT encoded by human diagnostic and therapeutic polynucleotide, and to
 PT induce antibodies
 PT
 PS Claim 2; SEQ ID No 573; 591pp; English.
 XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46652-ACC46749) and to their
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 CC to polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods
 CC of detecting dithp nucleotide and protein sequences; methods of
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridization
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and bacterial,
 CC proliferative disorders; autoimmune or inflammatory disorders; metabolic
 CC viral, fungal or parasitic infections; hormonal disorders; transport
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the effects of a tissue
 CC or cell type and to induce antibodies. The dithp therapy of the disorders
 CC mentioned above, as a source of antisense sequences of the disorders
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a dithp cDNA encoding a DITHP protein
 CC which is an organelle-associated protein.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIGO
 CC at ftp.wigo.int/pub/publshed_pcl_sequences.
 XX
 SO Sequence 2213 BP; 422 A; 751 C; 633 G; 407 T; 0 other;
 XX
 Alignment Scores:
 Pred. No.: 3,43e-157 Length: 2213
 Score: 1418.00 Matches: 277
 Percent Similarity: 96.22% Conservative: 5
 Best Local Similarity: 95.19% Mismatches: 5
 Query Match: 91.90% Indels: 5
 DB: 25 Gaps: 2
 US-09-811-094-33 (1-298) x ACC46652 (1-2213)
 QY 1 MetThrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaAla 20

```

Db      206 ATGACGAGAACAGCCATCTCTTCGCGCAAGACTTCTTGGCGGAGGCAATCGCGCGCC
Qy      21  IleserlysthrAlaValAlaProIleGluArgValIleLeuLeuGlnIleValGlnHis
Db      266 ATCTCCAAAGAGCGCGTGGCTCGATTCGAGCGGGTCAACCTCTGTCGAGGTCGCGAGC
Qy      41  AlaserlysglnIleAlaAlaAspIlysglnIlyrlysglyIleValAspCysIleValArg
Db      326 GCCACCAAGCAGATGCGCCCGCACAGCAGTACAAAGGCGATGCGATGCAATTCGCCG
Qy      61  IleProlysglnIleValIleuSerPheTrpArgGlyAsnIleuAlaAsnValIleArg
Db      386 ATCCCAAGAGAGCGGCGTGGCTCTGAGGGGCAACCTTCGCAACGTCATTCGC
Qy      81  TyrPheProThrGlnAlaLeuAsnPheAlaPheIlyAspIlyrlysglnIlePheLeu
Db      446 TACTTCCCACTCAAGCCCTCAACTTCGCTTCAAGAGTAAGTACAGACGATCTTCG
Qy      101 GilyGlyValAspIlyrlysthrGlnPheTrpArgGlyrlyPheAlaGlyAsnIleuAspGly
Db      506 GGGGCGGTGGACAGACACGACGAGTCTGGAGTACTTGGCGGCAACCTGGCGCTCGGC
Qy      121 GlyAlaAlaGlyAlaThrSerLeucySphValIlyrProLeuAspPheAlaArgThrArg
Db      566 GGTGGGCGCGCGGCGACCTCCCTGCTGCTGCTGACCCCTGGATTTCGCGCAAGCCGC
Qy      141 LeuAlaAlaAspValGlyIlyrlyserGlyrlyrGluArgGluPheArgIlyleuGlyAspCys
Db      626 CTGGCAGCGGAGCTGGGAAGTCAGCCACAGCCGAGATTCGAGCCCTGGAGAGCTGC
Qy      161 IleuValIlyrIleThrIlyrSerAspGlyIleArgGlyLeuIlyrGlnIlyrPheSerValSer
Db      686 CTGGTGAAGATACCAAGTCCAGCGCATCCGCGGCTTACCAAGGCTTACAGTGTCTCC
Qy      181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle
Db      746 GTGGCGGATCATCTTACCGGGGCGCTTCTGCGGTGATGATGCGGCAAGGCG
Qy      201 MetLeuProAspProIlyrlyAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal
Db      806 ATGCTCCCGGACCCCAAGAACAGCGCATCGTGTAGCTGATGATCCGCGAGACGCTG
Qy      221 ThrAlaValAlaGlyValIleSerIlyrProPheAspThrValIleArgIleArgMetMet
Db      866 AGCGCGGTGGCGCGGTGTCTCTACCCCTTCGACACGCTGGCGCGCATGATGATG
Qy      241 GlnSerGlyArgIlyrlysglyAlaAspIleMetIlyrThrGlyThrValAspCysTrpArgIly
Db      926 CAGTCCGGGCGCAAGAGACTGACATCATCATACGCGGCAACGTCGATGTTGGAGGAAG
Qy      261 IlePheArgAspGlnIlyrlyAlaPhePheIlysglyAla----Trp-----
Db      986 ATCTTCAGAGATGAGAGGGGCAAGGCTTCTTCAAGGGGTCAACACTGGAAACAAGGAGCG
Qy      276 ----SerAsnValIleuArgIlyrlyMetGlyIleValAla 285
Db      1046 CTCGCGGAGCGCTCGAGGGCTCACCTTCTGCA 1078

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XX      WO200175067-A2.
PN      11-OCT-2001.
XX      30-MAR-2001: 2001WO-US08631.
XX      31-MAR-2000: 2000US-0540217.
XX      23-AUG-2000: 2000US-0649167.
XX      (HYSE-) HYSEQ INC.
XX      Drmanac RT, Liu C, Tang YT;
XX      WPI: 2001-639362/73.
XX      P-Psdb; ABG27056.
PT      New isolated polynucleotide and encoded polypeptides, useful in
PT      diagnostics, forensics, gene mapping, identification of mutations
PT      responsible for genetic disorders or other traits and to assess
PT      biodiversity.
PS      Claim 1: SEQ ID No 27047; 103pp: English.
CC      The invention relates to isolated polynucleotide (I) and
CC      polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC      polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC      and gene mapping, and in recombinant production of (II). The
CC      polynucleotides are also used in diagnostics as expressed sequence tags
CC      for identifying expressed genes. (I) is useful in gene therapy techniques
CC      to restore normal activity of (II) or to treat disease states involving
CC      (II). (II) is useful for generating antibodies against it, detecting or
CC      quantitating a polypeptide in tissue, as molecular weight markers and as
CC      a food supplement. (II) and its binding partners are useful in medical
CC      imaging of sites expressing (II). (I) and (II) are useful for treating
CC      disorders involving aberrant protein expression or biological activity.
CC      The polypeptide and polynucleotide sequences have applications in
CC      diagnostics, forensics, gene mapping, identification of mutations
CC      responsible for genetic disorders or other traits to assess biodiversity
CC      and to produce other types of data and products dependent on DNA and
CC      amino acid sequences. AAS64197-AAS94564 represent novel human
CC      diagnostic coding sequences of the invention.
CC      Note: The sequence data for this patent did not appear in the printed
CC      specification, but was obtained in electronic format directly from WIPO
CC      at ftp.wipo.int/pub/published_pct_sequences.
SQ      Sequence 1156 BP; 264 A; 286 C; 302 G; 303 T; 1 other;
Alignment Scores:
Pred. No.: 1,81e-157 Length: 1156
Score: 1417.00 Matches: 274
Percent Similarity: 95.9% Conservative: 13
Best Local Similarity: 91.64% Mismatches: 9
Query Match: 91.83% Indels: 3
DB: 23 Gaps: 0
US-09-811-094-33 (1-298) x AAS91243 (1-1156)
Qy      1 MetThrGlnGlnAlaIleSerPheAlaIlyAspPheLeuAlaGlyIleAlaAla 20
Db      53 ATGACAGATGCCCTTGGCTCTTCCGCAAGGACTTCTTGGCAGGTGAGTGGCGGAGCC 112
Qy      21  IleserlysthrAlaValAlaProIleGluArgValIlyrlysglnIleValAspCysIleValArg 40
Db      113 ATCTCCAAAGAGCGCGGTAGCGCCATCGAGCGGGTCAAGTGTGCTGCGAGTGCAGCAT 172
Qy      41  AlaserlysglnIleAlaAlaAspIlysglnIlyrlysglyIleValAspCysIleValArg 60
Db      173 GCCACCAAGCAGATCCTCGATGATTAACAAGGCAATTAACAAGTGCAGTGCAGTGC 232
Qy      61  IleProlysglnIleValIleuSerPheTrpArgGlyAsnIleuAlaAsnValIleArg 80
Db      233 ATTCCAAGAGAGAGGAGTTCCTTCTTGGCGGTAACCTTGGCAATGTCATCAGCA 292

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OS Homo sapiens.

DB 514 CTGGCTGGGAGGTGGGAGGATCTTCCAGCAAGATTCATATGGCTGGGCGACTGT 573

QY 161 leuValylsIlethrylseraspilylearglyleutyrginglylpheserValSer 180

DB 574 CTCACCAAGATCTTCAAGTCGAGCGCCGGAAGGCTCTACAGAGGTTTCAGTCTCT 633

QY 181 ValGlnGlyIleIleIlethrylseraspilylearglyleutyrginglylpheserValSer 200

DB 634 GTCCAGGCGATCATATCATACAGAGCTGCTTCCGAGTGTATGACACTGCGCAAGGGG 693

QY 201 MetleuproaspProlylsasnThrHisIleValIleSerTrpMetIleIleVal 220

DB 694 ATGCTGCCAGACCCCAAGATGTGCATATCTGAGCTGATGATTTCCAGAGATGTG 753

QY 221 ThrAlaValAlaGlyValValSerTrpProheaspThrValArgArgMetMet 240

DB 754 ACAGCGCTGGCGGGCTGTCTTATCCGTTGACACTGTTGCTGCTGATGATGATGANG 813

QY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgLys 260

DB 814 CAGTCTGGCCGCAAGGGGCTGATATGTACAGGGGACCTGACTGCTGGAGGAG 873

QY 261 IlePheArgaspGlyGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280

DB 874 ATTGCAAAAGATGAAGAGCCCAACGCTTCTTCAAAAGTGTGCTGCTCAATGCTACTGAGA 933

QY 281 GlyMetGlyGlyAlaPheValIleuValIleuTrpAspGlyLeuLysValIle 298

DB 934 GGCATGGGCTGTCTTGTATGTATGATGATGATGATGATGATGATGATGATG 987

RESULT 15

AAV36480

ID AAV36480 standard; DNA; 1259 BP.

AC AAV36480;

DT 28-SEP-1998 (first entry)

XX Anti cDNA.

XX Anti: Adenine nucleotide translocator; cloning; screening;

KW DNA Tag diexoxy terminator cycle sequencing; oxidative phosphorylation;

KW probe: OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;

KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;

KW lactic acidosis; degenerative muscle disease; ss.

OS Mus sp.

XX Key Location/Qualifiers

FT CDS 190..1086

FT /tag- a

FT /product- "Anti protein"

XX MO9819714-Al.

XX 14-MAY-1998.

XX 31-OCT-1997; 97WO-US19882.

XX 01-NOV-1996; 96US-0030017.

XX (UYEM-) UNIV EMORY.

XX Graham BC, Macgregor GR, Wallace DC;

XX MPI; 1998-286608/25.

XX Mice lacking heart-muscle adenine nucleotide translocator protein -

XX useful as model for mitochondrial myopathy and hypertrophic

XX cardiomyopathy in animals and to test therapeutic compositions or

XX gene therapies

XX Disclosure; Page 40; 61pp; English.

XX The present sequence is a mouse Anti degenerate cDNA sequence, cloned

CC by screening a mouse heart cDNA library with the human Anti cDNA as a

CC probe. The Anti cDNA sequence was determined by DNA Tag diexoxy

CC terminator cycle sequencing. The Anti protein is encoded by the Anti

CC locus, a nuclear gene on chromosome 8. This protein is required in

CC mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP which

CC can then be converted into ATP. An Anti homozygous mutant would thus be

CC defective in OXPHOS which results in disease in oxidative metabolism

CC dependent tissues. This mouse Anti homozygous mutant can be used as a

CC model system for fascioscapular humeral muscular dystrophy, hypertrophic

CC cardiomyopathy, myopathy, lactic acidosis, etc. These model systems can

CC be used to test possible therapeutic compounds which increase/mediate ATP

CC and ADP exchange across the mitochondrial membrane independent of ADP1.

XX

SO Sequence 1259 BP; 274 A; 311 C; 339 G; 269 T; 66 other;

Alignment Scores:

Pred. No.:	5,35e-156	Length:	1259
Score:	1405.00	Matches:	263
Percent Similarity:	94.30%	Conservative:	18
Best Local Similarity:	88.26%	Mismatches:	17
Query Match:	91.06%	Indels:	0
DB:	19	Gaps:	0

US-09-811-094-33 (1-298) x AAV36480 (1-1259)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20

DB 190 ATGGGGATCAGGCTTGTAGCTTCTTAAAGACTTCTGCGAGTGGCATCGCGCGCC 249

QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40

DB 250 GTCTCCAGACGCGCGCTGCCCGCATCGAGAGGCTCAAACTGCTGCGAGCTCCAGCAT 309

QY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60

DB 310 GCCAGCAACAGATCATGTCAGAGAGAGAGATCAAAAGCATCTTATGTCGCGAGA 359

QY 61 IleProLysGluGlnIleValIleSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80

DB 370 ATCCCAAGAGAGAGGCTTCTCTCTTCTGAGGGGTACCTGGCCAAAGTATCCGG 429

QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100

DB 430 TACTCCCACTCAAGCCCTGAACTTGCCTTCAAAAGACAGACAGATCTTCTG 489

QY 101 GlyGlyValAlaAspLysHisTrpGlnPheTrpArgGlyPheAlaLysLeuAlaSerGly 120

DB 490 GGAGGGGTGATCGCATTAAGAGTTCGCGCTTACTTGTGCTGTAACCTGGGCTGTGT 549

QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTrpProLeuAspPheAlaArgThrArg 140

DB 550 GGGGCGAGCTGGGCGACCTCCCTGCTGCTTACCCGCTGACCTTGTGAGACAGG 609

QY 141 leuAlaAlaAspValAlaLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160

DB 610 CTGGCTGCCAGCTGGGCAAGGATCTTCCACAGCAAGAAATTCAAATGGGCTGGGCACTGT 659

QY 161 leuValLysIlethrylseraspilylearglyleutyrginglylpheserValSer 180

DB 670 CTCACCAAGATCTTCAAGTCGAGCGCCGGAAGGCTCTACAGAGGTTTCAGTCTCT 729

QY 181 ValGlnGlyIleIleIlethrylseraspilylearglyleutyrginglylpheserValSer 200

DB 730 GTCCAGGCGATCATCATCTACAGAGCTGCTTCCGAGTGTATGACACTGCGCAAGGG 789

QY 201 MetleuproaspProlylsasnThrHisIleValIleSerTrpMetIleIleVal 220

DB 790 ATGCTGCCAGACCCCAAGATGTGCATATCTGAGCTGATGATGATGATGATGATG 849

QY 221 ThrAlaValAlaGlyValValSerTrpProheaspThrValArgArgMetMet 240

Thu Aug 28 08:34:55 2003

us-09-811-094-33.p2n.rng

Page 16

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QY      241 GlnSerGlyArgGlySerGlyAlaAspIleMetTyrThrGlyValAspCysTyrPArgLys 260
Db      910 CAGTCTGCCCCGCAAGAGGGCGCTGATATGTATGTACACGGGACACTGTGACTGCTGAGAGAG 969
QY      261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTyrSerAsnValLeuArg 280
Db      970 ATTCGAAAGATGAGAGAGCCCAACGCTTCTTCAAGAGTGTGTCGCAATGTACTGAGA 1029
QY      281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
Db      1030 GGCAATGGGTGCTGTTCATTTGATGTATGTATGTATGATGATCAAAAAATATGTG 1083
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Search completed: August 27, 2003, 12:34:53
Job time : 343 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: August 27, 2003, 08:18:00 ; Search time 2281 seconds
(without alignments)
3175.245 Million cell updates/sec

Title: US-09-811-094-33
Perfect score: 1343
Sequence: 1 MTEGAISFANDFLAGIAAA.....LRGNGAFVLYDELKKVI 298

Scoring table:
BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 segs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-O=/cgn2.1/USPFO.spool.P/US09811094/runat.26082003.110450.8053/app.query.fasta.1.455
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-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR.SCORE=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09811094.ecgn.1.1.3549.etunat.26082003.110450.8053 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG.SCORES=0 -WAIT -DSPLOCK=100 -LONGIOG
-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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1: em_estba:*
2: em_esthum:*
3: em_estin:*
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8: em_hic:*
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10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	1355	11	BC013256
2	1543	100.0	1355	11	BC035469
3	1474	95.5	1201	13	BC419742
4	1463	94.8	1201	13	BC353661
5	1458	94.5	1201	9	AL545701
6	1454.5	94.3	1201	9	AL534908
7	1452.5	94.1	1071	12	BM554606
8	1451	94.0	949	13	BQ932832
9	1449	93.9	1201	9	AL540267
10	1445	93.6	1237	11	AK012751
11	1445	93.6	1237	11	AK088730
12	1445	93.6	1239	11	AK003467
13	1440	93.3	1015	13	BC360934
14	1436	93.1	1185	9	AL515693
15	1434	92.9	1201	13	BC424943
16	1432	92.8	1201	13	BC395578
17	1431	92.7	1045	13	BC420955
18	1418	91.9	1201	9	AL557414
19	1418	91.9	1201	13	BC462646
20	1416	91.8	1201	9	AL539376
21	1414	91.6	1295	11	AK078077
22	1405	91.1	1014	13	BC375536
23	1404	91.0	1090	13	BC457520
24	1400	90.7	931	13	BQ933670
25	1400	90.7	1201	9	AL514420
26	1388	90.6	1119	13	BU515488
27	1386	90.5	1209	14	CD496256
28	1393	90.3	1201	13	BC464683
29	1392	90.2	1236	11	AK002283
30	1389	90.1	999	13	BC411074
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32	1387	89.9	1030	12	BM476356
33	1385	89.8	1023	12	BM557479
34	1383	89.6	1201	13	BC439582
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36	1382	89.6	922	13	BQ226117
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43	1376	89.2	936	13	BU512229
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45	1375	89.1	973	13	BC447073

ALIGNMENTS

RESULT 1
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LOCUS BC013256 1355 bp mRNA
DEFINITION Homo sapiens, clone IMAGE:3865895, mRNA.
ACCESSION BC013256
VERSION BC013256.1 GI:15501544
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 1355)
Strausberg, R.

TITLE Direct Submission
JOURNAL Submitted (27-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: villalona@bcm.tmc.edu
Villalona, D.K., Luna, R.A., Hale, S.M., Huiyk, S., Lu, X., Garcia, A.M., Holloway, M., Telford, B., Hodgson, A., Boucek, J., Yu, W., Muzny, D.M., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 13 Row: e Column: 10
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 3820534
This clone has the following problem: no 5' EST match.

FEATURES
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/note="Vector: pCMV-SPORT6"

BASE COUNT 283 a 417 c 404 g 251 t
ORIGIN

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Score: 1543.00 Matches: 298
Percent Similarity: 100.008 Conservative: 0
Best Local Similarity: 100.008 Mismatches: 0
Query Match: 100.008 Indels: 0
DB: 11 Gaps: 0

US-09-811-094-33 (1-298) x BC013256 (1-1355)

OY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 92 ATACGGAAGAGGCGATCTCTGGCCAAAGACTCTTGGCCGAGGAGCATGCCGCCGCC 151
OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 152 ATCTCCAAAGCGCGTGGCTGCATGAGCGGGGTCAACCTCTCTGACAGTCAACAG 211
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 212 GCCAGCAACAGATGCCGCCGCGACAGCACTACAGGCGCATGTCGACTGATTCGCG 271
OY 61 IleProLysGluGluGlyValIleLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 272 ATCCCAAGAGGAGCGCGTGGCTCTCTCTGAGAGGGGCAACCTTGCCAAAGTATTCGC 331
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 332 TACTTCCCACTCAAGCCCTCACTGCGCTTCACAGATAGTACAAAGCAATCTTCTCG 391
OY 101 GlyGlyValAlaAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 392 GGGGCGCTGACACAGCAACGAGTCTGAGAGTACTTGGCGGCAACCTGCCCTCCGGC 451

OY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 452 GGTGGCGCGCGGCGACCTCCCTGCTGCTGTACCCGCTGGATTCGCGCAAGCCCG 511
OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 512 CTGGCAGCGCGAGCTGGGAAATCAGCAGCAGACCGGAGATTCGAGGCTGGGAGCTGG 571
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 572 CTGCTGAAGATACCAACAGATCCGAGCGCATCCGGGCGCTGTACAGGGCTTCAGTCTCC 631
OY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 632 GTGACAGGCGATCATCTACCGGGCGGCTTCTGCGGTGTACGATACGCGCAAGGCG 691
OY 201 MetLeuProAspProLysAsnThrHisIleValSerTyrPheMetIleAlaGlnThrVal 220
DB 692 ATGCTCCCGACCCCAAGACACACACATGCTGTGATGATGATCCGACACCGCTG 751
OY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgArgMetMetMet 240
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DB 872 ATCTTCAGATAGAGGAGGCGAGCTCTTCTCAAGGTCGCTGCGCAAGTCTCGGG 931
OY 281 GlyMetCylGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 932 GGCATGGGGGCGCGCTTCTGCTGCTGTGACACAGCTCAAGAGGTATATC 985

RESULT 2
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LOCUS
DEFINITION Homo sapiens, clone IMAGE:3867130, mRNA.
ACCESSION BC035469
VERSION BC035469.1 GI:22028373
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM

REFERENCE
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgaps-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center
Center code: BCM-HGSC
Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
Contact: amg@bcm.tmc.edu
Gunnarone, P.H., Garcia, A.M., Lu, X., Huiyk, S.M., Hale, S.M., Yoon, V.S., Kowis, G.R., Lawrence, S., Martin, R.G., Muzny, D.M., Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 13 Row: f Column: 9
This clone was selected for full length sequencing because it

Db 212 ATCTCAAGAGCGCCCTGGCTCCAGTCAGCGGCTACAGCTGCTGTCAGTCCAGCAGC 271
 Oy 41 AAlaserlysglnlleaAlaAlaAspLysGlnTyrLysGlylleValAspCyslleValArg 60
 Db 272 GCCAGCAAGCAGATCCCGCCCGCACAGATACAGAGCGCTCTGACGACGCTGCTCCG 331
 Oy 61 IleProlysglnGlnGlyValIleuSerPheThrArgGlyValIleuAlaAsnValIleArg 80
 Db 332 ATCCCAAGAGCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 391
 Oy 81 TyrPheProThrGlnAlaIleuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 392 TACTTCCCACTACAGCCCTCAACTTCCCTTCAAGATACAGATACAGATACAGATACAG 451
 Oy 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 452 GGGGCGCGGACAGACAGACAGCGCTTGGAGTACTTGGGGCAACCTGGCGCTCCGGC 511
 Oy 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaThrArg 140
 Db 512 GGTGGCGCGCGGAGCT 571
 Oy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 572 CTGGCAGCGGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 631
 Oy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 632 CTGCTGAGATCACCAGATCCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 691
 Oy 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLys 200
 Db 692 GTGCGAGGATCATACATACATACATACATACATACATACATACATACATACATACAT 751
 Oy 200 YmetLeuProAspProLysAsnThrHisIleValAlaSerThrPheIleAlaGlnThrVa 220
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 Oy 220 LThrAlaValAlaGlyValAlaSerTyrProPheAspThrValAlaArgArgMetMet 240
 Db 812 GACG 871
 Oy 240 TglnSerGlyArgGlyAlaAspIleMetTyrThrGlyThrValAlaAspCysThrArg 260
 Db 872 GCAGTCG 931
 Oy 260 sIlePheArgAspGlnGlyLysAlaPhePheLysGlyAlaTyrPheSerAsnValLeu 280
 Db 932 GATCTTCACAGATGAGGGGGGCGAGGCTTCTTCAAGGGTGGTGTCTCAACGCTGCG 991
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 VERSION BK353661.1 GI:30375795
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 ORGANISM Homo sapiens
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 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1. (bases 1 to 1201)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 11066.f. For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0DC0101K03&cluster=11066.f. Contact:
 Feng Liang Email: fliang@life.com URL:
 http://fulllength.invitrogen.com/Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID: CS0DC0101K02P1.
 Location/Qualifiers
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 /note="1st strand cDNA was primed with a NotI-oligo(dT)
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 digested with Not I and cloned into the Not I and EcoR V
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BASE COUNT 282 a 281 c 301 g 265 t 72 others
 ORIGIN

Alignment Scores:
 Pred. No.: 3, 6e-172 Length: 1201
 Score: 1463.00 Matches: 275
 Percent Similarity: 97.308 Conservative: 13
 Best Local Similarity: 92.918 Mismatches: 8
 Query Match: 94.828 Indels: 0
 DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BK353661 (1-1201)

Oy 1 MethrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAlaAla 20
 Db 128 ATGACATATCGCGCTGTGCTTCCCGCAAGAGATCTCTGAGAGTGGAGCGCAGCC 187
 Oy 21 TleSerTyrThrAlaValAlaProIleGluArgValLysLeuLeuGlnAlaGlnHis 40
 Db 188 ATCTCCAAAGCGCGGTACGCCCATGAGCGGCTCAAGCTGCTGTCAGAGTGCAGCAT 247
 Oy 41 AAlaserlysglnlleaAlaAlaAspLysGlnTyrLysGlylleValAspCyslleValArg 60
 Db 248 GCACGACAGCAGATCAGTCACTGATACCAATCAAGCATTTATAGCTGCTGCTGCT 307
 Oy 61 IleProlysglnGlnGlyValIleuSerPheThrArgGlyValIleuAlaAsnValIleArg 80
 Db 308 ATCCCAAGAGCAGGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 367
 Oy 81 TyrPheProThrGlnAlaIleuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 368 TACTTCCCACTACAGCCCTCAACTTCCCTTCAAGATACAGATACAGATACAGATACAG 427
 Oy 101 GlyGlyValAspLysHisThrGlnPheThrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 428 GGTGCTGCGCAAGAGAGATCTTGGCGCTTACCTTCAAGATACAGATACAGATACAG 487
 Oy 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaThrArg 140
 Db 488 GGTGCGCGGAGGAGCAATCCCTGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 547
 Oy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
 Db 548 CTAGCGCTGATGCGGTAAACTGAGCTGAAGAGGAAATCCAGAGCCCTGGCTGCTC 607
 Oy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 608 CTGCTTACATCTCAAAATCGATGAGGATTAAGGCGCTGACCAAGCTTAACTGCTCT 667
 Oy 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 668 GTGCGAGGATTTATCATCTACAGCGCGCTTACTTGTATCATGACACTGCAAGAGGA 727

OY	201	MelleuprOApSPpOLyASaNTThiArlleValaValSeRTpMctIleAlaGlnThrVal	220
Db	728	ATGCTTCGGATCCCAAGACACACACATCCATCCATCCACTGGATGATGCGACAGACTTC	787
OY	221	ThraValaValaValaValaValSeRTyrTrpObheAspThrValaArgArgMetMet	240
Db	788	ACTCTGTGTGGCGGGGTGACTTCTCATTCATTGGACACCTGTGGCGCGCATGATGATG	847
OY	241	GlnSerGlyAtrGlySSGlyAlaAspIleMetYrThrGlyThrValaAspCysTTrpArgS	260
Db	848	CAGTCACAGGGCCAAAGGACACTGACATCATCTGTACACAGGACAGCTTGATGCTGGGGAG	907
OY	261	IleObheArGAspGlnGlyGlyLyAlaObheObheLySGlyAlaTrpSerAsnValLeuArg	280
Db	908	ATTCTCGTGATGAAAGGCGCAAGCTTTTTCAGGGGTGATGATGCCAATGTTCTCAGA	967
OY	281	GlyMetGlyGlyAlaObheValLeuValLeuYrAspGluLeuValSlyS	296
Db	968	GCGATGGGTGGCTTATGTGCTGTGCTGTATGATGATGAATCAAGAAAG	1015

RESULT	5	AL545701	LOCUS	DEFINITION
	AL545701	1201 bp	1linear	EST 31-MAY-2003
	AL545701	Homo sapiens PLACENTA COT 25-NORMALIZED	Homo sapiens cDNA	
	clone GSD01009YH03 5-PRIME	mRNA sequence.		

VERSION	AL545701.2	GI:31267536
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Contact: Genoscope
Genoscope - Centre National de Séquençage
BP 191 91006 Evry cedex - France
Email: segret@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10389.i For
more information about this cluster, see
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgt-bin/cluster.cgi?seq=CSD01009CD020P1&cluster=10389.i)
Feng Liang Email : liang@lifestech.com URL : <http://fulllength.invitrogen.com/> Invitrogen 1600
Faraday Avenue Genoscope sequence ID : CSD01009CD020P1.

FEATURES	SOURCE	Location/Qualifiers
		1..1201
		/organism="Homo sapiens"
		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/clone="CSDD1009YH03"
		/tissue_type="PLACENTA COT 25-NORMALIZED"
		/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
		/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
BASE COUNT		248 a 362 c 372 g 218 t
ORIGIN		1 others

Alignment Scores:	
Pred. No.:	1.52e-171
Score:	1458.00
Percent Similarity:	97.37%
Best Local Similarity:	96.99%
Query Match:	94.49%
DB:	9
	Gaps: 0
	Length: 1201
	Matches: 290
	Conservative: 1
	Mismatches: 6
	Indels: 3
	Gaps: 0

US-09-811-094-33 (1-298) x AL545701 (1-1201)

QY	2	ThrGlnGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaIle	21
Db	51	TCCGGGATGCATCTCTCTGGCCAAAGACTTCTGGCGGACGGCTNCGCGCGCCATC	110
QY	22	SerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAla	41
Db	111	TTCAGAGAGGGCGGTGGCTCCATGCACGAGGGGTCAGCGTGGCTCCAGTCAGCAAGCC	170
QY	42	SerLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleLeuArgIle	61
Db	171	AGCAAGCAGATCGCCCGGACAGCAGTACAGGSCATCGTGAATGCTATTCGGCATC	230
QY	62	ProLysGlnGlnGlyValLeuSerPheTrpArgLysAlaLeuAlaAsnValIleArgTrp	81
Db	221	CCCAAGGAGCAGGGCGGTGCTGCTCCCTTCGAGGGGCAACCTTGCCAAAGTATTCGTAC	290
QY	82	PheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeuGly	101
Db	231	TTCGCCACTCAGCCCTCACTCGCCCTTCAGAGTAAAGTCAACACAACTCTCTCGGGG	350
QY	102	GlyValAspLysHisThrGlnPheTrpArgTrpPheAlaGlyAsnLeuAlaSerGlyGly	121
Db	351	GGCGTGGACAAAGCACACGACAGTTCGGAGTACTTGGGGGCAACTGGCCCTCGGGCGT	410
QY	122	AlaAlaGlnAlaThrSerLeuCysPheValIlyProLeuAspPheAlaArgThrArgLeu	141
Db	411	GCGCGCGCGGACCTCCCTGCTGCTGTGATCCGCGGAAATTCGCCAAGACCCGCGTG	470
QY	142	AlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCysLeu	161
Db	471	GCAGGGGACGTGGGAAAGTCAGGCACAGACGCCGAGTTCGAGGCGCTGGAGACTGCGCTG	530
QY	162	ValLysIleIleThrLysSerAspGlyIleArgGlyLeuTrpGlnGlyPheSerValSerVal	181
Db	531	GTAAGATACACCAAGTCCGACGCGCATCCGGGGCCGTGCACAGGGCTTCAGTCTCCCGTG	590
QY	182	GlnGlyIleIleIleTrpArgAlaAlaIleTrpPheGlyValIlyTrpAspThrAlaLysGlyMet	201
Db	551	CAGGCGATCATCATTTACCGGGCGGCTCACTTCGGCGGTGATGAGATACGGCCAAAGGCATG	650
QY	202	LeuProAspProLysAsnTrpHisIleValValSerTrpMetIleAlaGlnThrValThr	221
Db	651	CTCCCGGACCCCAAGAACACGACACATCGTGGAGACTGATGATCGCGACACGCTGACG	710
QY	222	AlaValAlaGlyValValSerTrpProPheAspThrValArgArgMetMetLeuGln	241
Db	711	GCGGTGGCGGGGTGGTGTCTTACCCCTTCGACGAGGGGGCGGCGCATGTGATGTCAG	770
QY	242	SerGlyArgLysGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgLysIle	261
Db	771	TCCGGGCGCAAAAGAGCTGACATCATGTACAGGGCAGCTC-GACTGTTCGAGGAAGATC	829
QY	262	PheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaIleTrpSerAsnValLeuArgGly	281
Db	830	TTCACAGATGAGGGGGGCAAGCGCTTCCTTCAGAGGTGGCTGCTCCAACTCTCGGGGCG	889
QY	282	--MetGlyValaPheValLeuValLeuValTrpAspGluLeuLysLysValIle	298
Db	890	CATGGGGGGGCCCTTCGTGCTGTGCTTCGTACGACGACTCAAGAAAGTGATC	942

RESULT 6	AL534908	1201 bp	mRNA	linear	EST 12-MAY-2001
LOCUS	AL534908				
DEFINITION	AL534908 Homo sapiens FETAL BRAIN Homo sapiens CDNA clone CS00F007Y120 5-PRIME, mRNA sequence.				
ACCESSION	AL534908				
VERSION	AL534908.2	GI:30541165			
KEYWORDS	EST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				

BASE COUNT 214 a 335 c 334 g 187 t 1 others
 ORIGIN

Alignment Scores:
 Pred. No.: 6,26e-171 Length: 1071
 Score: 1452.50 Matches: 292
 Percent Similarity: 97.34% Conservative: 1
 Best Local Similarity: 97.01% Mismatches: 3
 Query Match: 94.13% Indels: 5
 DB: 12 Gaps: 1

US-09-811-094-33 (1-298) x BM554606 (1-1071)

QY 1 MetThrGluGlnAlaIleSerPheAlaIleAspPheLeuAlaGlyIleAlaAla 20
 Db 13 ATGACGGAACAGCGCCATCTCCGCAAAAGACTTCTGGCGAGGACATCGCGCGCC 72

QY 21 IleSerIleThrAlaValAlaProIleGluArgValIleLeuLeuGlnValGlnHis 40
 Db 73 ATCTCCAGAGCGCGCTGCTCGATCGAGCGGGTCAGAGCTGCTGCTGCGAGTCCAGCAC 132

QY 41 AlaSerIleGlnIleAlaAlaAspIleGlnIleValIleValAspCysIleValArg 60
 Db 133 GCGAGCAAGAGATGCCCGCGCGACAGAGTACAGAGGCAATCGTGAGTCAATGTCGCC 132

QY 61 IleProIleGluGlnIleValIleLeuSerPheTrpArgIleValIleValIleArg 80
 Db 193 ATCCCAAGAGAGCGCGCTGCTGCTGAGGGGCAACCTTGCGCAACGTCATTCGCG 252

QY 81 TyrPheProThrIleAlaLeuAsnPheAlaPheIleAspIleValIlePheLeu 100
 Db 253 TACTTCCCACTCAACCCCTCAACTCTGCTTCAAGATTAAGTCAAGACAGATCTTCG 312

QY 101 GlyIleValAspIleThrIleGlnPheTrpArgIlePheAlaGlnIleValIleSer 120
 Db 313 GGGGGGTGACAGACAGACAGAGTCTGAGTACTTTCGGGCAACCTGCGCTCGCGC 372

QY 121 GlyAlaAlaGlyIleThrSerIleValIleValIleValIleValIleValIleVal 140
 Db 373 GGTGGCGCGCGCGCGACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 432

QY 141 LeuAlaAlaAspIleGlnIleValIleValIleValIleValIleValIleValIle 160
 Db 433 CTGCGAGCGAGCTGGGAAAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 492

QY 161 LeuValIleIleThrIleSerIleValIleValIleValIleValIleValIleVal 180
 Db 493 CTGCTGAGATCAACCAAGTCCGAGCGCATCGGGGCTGTACAGAGCGCTTCAAGTCTCC 552

QY 181 ValGlnGlyIleIleIleIleIleIleIleIleIleIleIleIleIleIleIleIle 200
 Db 553 GTCCAGAGGCAATCATCTACCGCGCGCTACTTGGCGGTGATACATGAGGCAAGGCG 612

QY 201 MetLeuProAspProIleAsnThrHisIleValIleValIleValIleValIleVal 220
 Db 613 ATGCTCCCGACCCCAAGACAGACAGCATGTGTGAGTGGAGTGGAGTGGAGTGG 672

QY 221 ThrAlaValAlaGlyValIleSerIleValIleValIleValIleValIleValIle 240
 Db 673 AGGCGCGTGGCGCGCGGTGCTCTTCCATCCCTTGCAGACGATCGCGCGCGCATATG 732

QY 241 GlnSerIleValIleGlyIleAlaAspIleMetIleThrIleValIleValIleValIle 260
 Db 733 CAGTCCGCGCGCAAGAGAGTGTACATCATGTACAGGCGACCGTCACTGTGGAGGAA 792

QY 260 sIlePheArgAspGlu-GlyIleValIleValIleValIleValIleValIleValIle 279
 Db 793 GATCTTCAGAGATGAGGGGGGCAAGGCTTCTTCAAGGGGCTGGGCTCCAAAGTCTG 852

QY 280 ArgGlyMetGlyIleValIle--PheVal-LeuValIleValIleValIleValIleVal 296
 Db 853 CGGGGGGATGGGGGGCGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 907

RESULT 8
 BQ932832
 LOCUS
 DEFINITION
 AGENCOURT_8824122 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:6459460
 5', mRNA sequence.

ACCESSION
 BQ932832
 VERSION
 BQ932832.1 GI:22348215
 KEYWORDS
 EST.
 SOURCE
 Homo sapiens (human)
 ORGANISM
 Homo sapiens

REFERENCE
 1 (bases 1 to 949)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-remail.nih.gov
 Tissue Procurement: DCTD/DTF/Gazdar
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
 Plate: LNCM2644 row: 3 column: 05
 High quality sequence stop: 674.
 Location/Qualifiers

FEATURES
 source
 1..949
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6459460"
 /tissue_type="large cell carcinoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH-MGC_18"
 /note="Organ: Lung; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGGCAGGCG(5). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH-MGC Library."

BASE COUNT 172 a 305 c 297 g 173 t 2 others
 ORIGIN

Alignment Scores:
 Pred. No.: 8.04e-171 Length: 949
 Score: 1451.00 Matches: 285
 Percent Similarity: 96.98% Conservative: 4
 Best Local Similarity: 95.64% Mismatches: 7
 Query Match: 94.04% Indels: 2
 DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x BQ932832 (1-949)

QY 1 MetThrGluGlnAlaIleSerPheAlaIleAspPheLeuAlaGlyIleAlaAla 20
 Db 53 ATGACGGAACAGCGCCATCTCCGCAAAAGACTTCTGGCGAGGACATCGCGCGCC 112

QY 21 IleSerIleThrAlaValAlaProIleGluArgValIleLeuLeuGlnValGlnHis 40
 Db 113 ATCTCCAGAGCGCGCTGCTCGATCGAGCGGGTCAAGTCTGCTGAGTCCAGGAC 172

QY 41 AlaSerIleGlnIleAlaAlaAspIleGlnIleValIleValAspCysIleValArg 60
 Db 173 GCGAGCAAGAGATGCCCGCGCGACAGAGTACAGAGGCAATCGTGAGTCAATGTCGCC 232

QY 61 IleProIleGluGlnIleValIleLeuSerPheTrpArgIleValIleValIleValIleArg 80
 Db 233 ATCCCAAGAGAGCGCGCTGCTGCTGAGGGGCAACCTTGCGCAACGTCATTCGCG 292

OY		81	lyrPhePrOThrcGlnAlaLeuAnpHelaPhelAysAspLyfRyLysGlnIlePheLeu	100
Db		293	TACTTCCCACTCAAGCCTCAATTCCTCCCTCAAGATAAAGTAACAAGCATCTCTCG	352
OY		101	GlyGIyValAspLysHisThrGlnPheTrpArgTyPheAlaGlySnuLeuAlaseryl	120
Db		353	GGGGCGCGGACGAAGCACACAGAGTTCTGGAGGTACTTTGGGGCAACTGGGCCTCGGC	412
OY		121	GlyAlaAlaGlyAlaThrSerLeucPheValTyProLeuAspPheAlaArgThrArg	140
Db		413	GGTGCGCGCGCGGACCCTCCCTGCTCTGTTGCCGGTGGATTTCGCCAAMACCGC	472
OY		141	LeuAlaAlaAspValGlyLysSerGlyThrGluArgLutPheArgGlyLeuGlyAspCys	160
Db		473	CITGGACGCGGACGTGGGMAAGTCAGGCACAGACGCGGATTCGAGGCTGGAGAGCTCC	532
OY		161	LeuValLysIleIleThrLysSerAspCylIleAsgGlyLeuTyrgInglyPheSerValser	180
Db		533	CTGGTAGAGATCACCAAGATCCGACGCGCATCCGGGCGCTGTACCGAGGCTCAATGTCTCC	592
OY		181	ValGlnGlyIleIleIleTyArgAlaAlaIleTyPheGlyValTyAspThrAlaLysGly	200
Db		593	GTCAGAGGCATCATCATCTACCGGGCGGCTACTTCGGCGGTACGATACGGCCAAGGGC	652
OY		201	MetLeuProAspProLysAsnThrHisIleValIleSerTPMetIleAlaGlnThrVal	220
Db		653	ATCGTCCCGACCCCAAGAACACGACATCGTGGTAGCTGAATGATCCGCGAGACCGTG	712
OY		221	ThrAlaValAlaGlyValIleSerTyProPheAspThrValArgArgGlyMetLcmet	240
Db		713	ACGGCCGTGGCGCGCTGTCTCTACCTTGACACGCTCGGGCGCGCATGATGATG	772
OY		241	GlnSerGlyArgLysGlyAlaAspIleMetTyThrGlyThrValAspCys-TyrArgTy	260
Db		773	CAGTCGCGGGCGAAGAGACTGACATCATGTACACGGGACCGCTGCATGCTGTGAGAAG	832
OY		260	AlaPheArgAspGluGlyGlyValAlaPhePheLysGlyAlaTrpSerAsnValLeuar	280
Db		833	GATCTTCANAGATGAGGGGGCGGCTTCTTCMAAGGTGGCTGTGCACGCTCGTCNG	892
OY		280	GgLYMeTgLYGlyAla-PheValLeuValLeuTyRaspGLueuLysLys	296
Db		893	GGGCATGGGGGGCGCCCTTCGTGCTGTCGACGACGAACTCAAGG	942
RESULT 9				
AL540267		1201 bp	mRNA	linear EST 31-MAY-2003
LOCUS	AL540267 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone			
DEFINITION	CSDFP032YN01 5'-PRIME, mRNA sequence.			
ACCESSION	AL540267			
VERSION	AL540267.2 GI:31264828			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1. (bases 1 to 1201) Li,W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished			
AUTHORS	contact: genoscope			
TITLE	Genoscope - Centre National de Sequencage			
JOURNAL	BP 191 91006 Evry cedex - France			
COMMENT	Email: seqref@genoscope.cns.fr Web : www.genoscope.cns.fr was not normalized. Library was constructed by Life Technologies, division of Invitrogen. This sequence belongs to sequence cluster 10389.f for more information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq-CSDFP032CG010PLICluster=10389.f . Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ INVitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSDFP032CG010Pl.			

FEATURES
SOURCE

Location/Qualifiers
1. .1201

BASE COUNT
ORIGIN

349 C	331 g	210 C	20 C
-------	-------	-------	------

Alignment Scores:	
Pred. No.:	2,04e-170
Score:	1449.00
Percent Similarity:	98.96%
Best Local Similarity:	98.96%
Query Match:	93.91%
DB:	9
	Gaps: 0
	Matches: 1201
	Conservative: 0
	Mismatches: 2
	Indels: 3
	Gaps: 0

US-09-811-094-33 (1-298) x AL540267 (1-1201)

[illegible]

	Oy	818	ACGCCGTGGCGGCTGCATCCCTTCAGACAGTGCGGGCAGCATANTG	877
	JOURNAL TITLE	241	GlnSerGlyAlrGylSglYalAaplleMettTyrHnGlyThvAlspCystrPrArgLys	260
	PUBMED MEDLINE	878	CAGTCCGGGGCAAGAAGACTCACATCATGTAACAGGGGCGGCTGTTGGAGGAAG	937
	Oy	261	IlePharAspelunGlYgLySalaphelpelySGlYalaTrtserASValLeunrg	280
	Db	938	ATTCTTAGAGATGAGGGGGGCAAGGCTTCTTCAAAGGGGGCTGTTCCAACGCTCGGG	997
	Db	281	GlyMetClYglYalApheVallenuAl	289
	LOCUS AK012751	998	GGCATGGGGGGSC-TTCGTGCTGGTC	1023
	RESULT 10			
	DEFINITION	AK012751	1237 bp mRNA linear HTC 05-DEC-2002 Mus musculus 10, 11 days embryo whole body cdna, RIKEN full-length enriched library, clone:2810016m09 product:solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5, full insert sequence.	
	VERSION	AK012751.1	GI:12849699	
	SOURCE KEYWORDS	HTC; CAP trapper.	Mus musculus (house mouse)	
	ORGANISM		Buckaryaota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
	REFERENCE AUTHORS	1	Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 10349636	
	TITLE	2	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shihata,K., Itoh,M., Kono,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected CDNA's to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159	
	JOURNAL PUBLISHED	3	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Kono,H., Ariyasu,J., Nishi,K., Kitsumai,T., Tashiro,H., Itoh,M., Sumi,I., Ishii,Y., Nakamura,S., Hazama,M., Nishino,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kasahagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watabiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsumura,S., Kawaji,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kita,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Sequence Res. 10 (11), 1757-1771 (2000)	
	TITLE	4	Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,D.A., Fukunishi,Y., Kono,H., Adachi,J., Fukuda,S., Aizawa,K., Kamiya,M., Nishi,K., Miyasawa,H., Kondo,S., Yananaka,I., Salto,T., Okazaki,Y., Gojobori,T., Bono.H., Kasukawa,T., Salto.R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Glass,C., Kling,B., Kochiya,H., Klehl,P., Lewis,S., Matsuo.Y., Nikaido,I., Pesole,G., Quackenbush.J., Schriml,L.M., Staudil,F., Suzuki,R., Tomita,M., Wagner,L., Washio.T., Sakai.K., Okido,T., Furuno.M., Aono.H., Baldarelli,R., Barsh.G., Blake,J., Boffelli.D., Bojunga.N., Carninci.P., de Bonaldo.M.F., Brownstein.M.U., Bul.C., Fletcher.C., Fujita.M., Gariboldi.M., Gustincich.S., Hill,D., Hofmann.M., Hunne.D.A., Kamiya.M., Lee.N.H., Lyons.P., Marchionni.L., Mashima.J., Mazzarello.I., Mombeats,P., Nordone.P., Rato.K., Ringwald.M., Rodriguez.I., Sakamoto.N., Sasaki.H., Sato,K., Schonbach.C., Seya.T., Shibata.Y., Storck,K.F., Suzuki.H., Toyo-Oka,K., Wang,K.H., Weitz,C., Whitaker.C., Wilming.L., Wynshaw-Boris.A., Yoshida,K., Hasigawa,Y., Kawaji.H., Kontsutki.S. and Hayashizaki,Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 PUBMED MEDLINE 11217851	
	FEATURES SOURCE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (phase 1 to 1237) Arakawa,T., Aizawa,K., Akabira,S., Akimura,T., Ara,i.A., Aono,H., Atakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu.N., Hiramoto,K., Hirotsuka,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Koijma,Y., Kono.H., Kouda.M., Koya,S., Kurihara,C., Matsuyama,T., Miyezaki,A., Nishi,K., Nomura,K., Numazaki,R., Onno.M., Okazaki,Y., Okido.T., Owa.C., Salto,H., Salto,R., Sakai,C., Sakai,K., Sano,H., Sasaki.D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi.F., Tanaka,T., Tejima,Y., Toyta.T., Yamamura.T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y. Direct Submission Submitted (10-JUN-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel.:81-45-503-9222, Fax:81-45-503-9216) Please visit our web site (http://genome.gsc.riken.go.jp/) for further details. cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGATCCAAAGCGCTTTTTTTTTTTTTTTVN 3'] [5' GAGAGAGAGAGATCCAAAGCGCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 7.5 and subtraction to Rot = 37.5. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATCCGACGTTAAATAATATCCCCCCCOC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOIR. Location/Qualifiers 1..1237 /organism="Mus musculus" /mol_type="mrna" /strain="C57BL/6J" /db_xref="FANTOM_DB:2810016M09" /db_xref="MG1:1899048" /db_xref="taxon:10090" /clone="2810016M09" /tissue-type="whole body" /clone_lib-"RIKEN full-length enriched mouse cDNA library" /dev_stage="10, 11 days embryo" 79..975 /note="Unamed protein product; putative solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 (MDIMGI:1353496)" /codon_start=1 /protein_id="BAB28445.1" /db_xref="gi:12849700" /db_xref="MG1:1353496" /translation="MTDAVSARXKFLAGVAALISRTAVPRVKLLIOVOHASKO LTRDKRYKITGVPIKEQCVLSFMGNLANAYRRPPQAAPARKDRLQLFDLG VNRITDFMRFTNGNLASGGAATSLCYTPIDPAKTPLADVDKAAGEEFKKGLGDC LVNRTSDSKIGLYOGFNSSVGIIIVRAAFGYIDRAKMLDPKRTHIFTSMIWLO"	

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		REFERENCE	
		1 Carninci, P. and Hayashizaki, Y.	
		High-efficiency full-length cDNA cloning	
		Meth. Enzymol. 303, 19-44 (1999)	
		99279253	
		10349636	
		2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,	
		Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.	
		Normalization and subtraction of cap-trapper-selected cDNAs to	
		prepare full-length cDNA libraries for rapid discovery of new genes	
		Genome Res. 10 (10), 1617-1630 (2000)	
		2049374	
		11042159	
		3 Shibata, K., Itoh, M., Aizawa, K., Nagakura, S., Sasaki, N., Carninci, P.,	
		Kono, H., Akiyama, J., Nishi, K., Kitanai, T., Tashiro, H., Itoh, M.,	
		Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,	
		Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,	
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		Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,	
		Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.	
		Riken integrated sequence analysis (RISA) system-384-format	
		sequencing pipeline with 384 multiplexed capillary sequencer	
		Genome Res. 10 (11), 1757-1771 (2000)	
		20530913	
		11076861	
		4 Kawai, J., Shimagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,	
		Aizawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S.,	
		Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamada, J.,	
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		Quackenbush, J., Schriml, L. M., Staudl, F., Suzuki, K., Tomita, M.,	
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		Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D.,	
		Hofmann, M., Hume, D. A., Kamlay, M., Lee, N. H., Lyons, P.,	
		Meroni, L., Mashima, J., Mazzarelli, J., Momberechts, P., Nordone, P.,	
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		Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohatsu, S.,	
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		Nature 409 (6821), 685-690 (2001)	
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		5 The FANTOM Consortium and the RIKEN Genome Exploration Research	

TITLE	Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
REFERENCE	6 (bases 1 to 1237)
AUTHORS	Adachi,J., Aizawa,K., Akimura,T., Aikawa,T., Bono,H., Carninci,P.

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 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 1015)
 AUTHORS Li, W.-B., Gruber, C., Jessee, J., and Polyes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT Contact: Genoscope

Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 11066.f For
 more information about this cluster, see
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 Feng Liang Email : fliang@life.techn.com url :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
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Listing first 45 summaries

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-DEV.TIMEOUT=120 -WARN.TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database : Issued_Patents_NA:*

1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PTUS.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1543	100.0	897	4	US-09-434-354-3
2	1543	100.0	1212	4	US-09-620-312D-687
3	1454	94.2	897	4	US-09-434-354-2
4	1412	91.5	1177	3	US-08-961-871-9
5	1405	91.1	1259	3	US-08-961-871-11
6	1385.5	89.8	894	4	US-09-434-354-1
7	314	20.3	3334	4	US-09-996-243-288
8	311	20.2	1816	3	US-09-188-930-262
9	311	20.2	1816	4	US-09-312-283C-262
10	299.5	19.4	2663	4	US-09-620-312D-283
11	294	19.1	289	4	US-09-016-434-622
12	286	18.5	1674	4	US-09-482-273-26

13	283.5	18.4	876	4	US-09-501-558-1
14	280	18.1	1443	4	US-09-160-119-3
15	280	18.1	2095	4	US-09-160-119-1
16	265	17.2	1192	3	US-09-142-565-1
17	250.5	16.2	1255	1	US-08-518-878B-38
18	250.5	16.2	1255	1	US-08-294-522B-38
19	250.5	16.2	1255	2	US-08-470-868A-38
20	250.5	16.2	1596	2	US-08-807-861A-38
21	250.5	16.2	1596	3	US-09-210-681-38
22	250.5	16.2	1596	3	US-08-946-719A-38
23	250.5	15.9	1596	4	US-09-547-983-38
24	245	15.9	1949	2	US-08-937-466-3
25	245	15.9	1949	2	US-09-172-528-3
26	245	15.9	1949	3	US-09-318-199-3
27	245	15.9	1949	3	US-09-503-579-3
28	244	15.8	2782	2	US-08-937-466-1
29	244	15.8	2782	2	US-09-172-528-1
30	244	15.8	2782	3	US-09-318-199-1
31	244	15.8	2782	3	US-09-503-579-1
32	239.5	15.5	1764	4	US-09-620-312D-548
33	233.5	15.1	1594	2	US-08-933-750C-61
34	233.5	15.1	1594	3	US-08-933-750C-61
35	230	14.9	1679	4	US-09-620-312D-997
36	228.5	14.9	1566	4	US-09-620-312D-63
37	227.5	14.7	1205	1	US-08-518-878B-36
38	227.5	14.7	1205	1	US-08-294-522B-37
39	227.5	14.7	1205	2	US-08-807-861A-36
40	227.5	14.7	1205	2	US-08-470-868A-36
41	227.5	14.7	1205	3	US-09-210-681-36
42	227.5	14.7	1205	3	US-08-946-719A-36
43	227.5	14.7	1205	4	US-09-547-983-36
44	222	14.4	882	4	US-09-501-558-3
45	214	13.9	1341	4	US-09-620-312D-207

ALIGNMENTS

RESULT 1
US-09-434-354-3
Sequence 3, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri, Luciano G.
APPLICANT: Vellelebl, Gonul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660086.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapiens
US-09-434-354-3
Alignment Scores:
Pred. No.: 9.07e-180
Score: 1543.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 4
Gaps: 0
Matches: 897
Conservative: 298
Mismatch: 0
Indels: 0

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Qy 181 valginglyllellelletyrargalaalaatyrpneglvaltyraspthralalysgly 200
Db 671 GTGACGGGATCATCATCTACCGGGGCTTACTTCCGGGGTGTACGATACGGCCAAAGGC 730
Qy 201 Metleuproasprrpolsasnthrhsllevalvalsertrpmetllealaglnthval 220
Db 731 ATGTCCTCCCGACCCCAAGACACGACATCGTGTGAGCATGATGATCGCGACGACCGTG 790
Qy 221 ThrAlaValAlaGlyValValSerTyrPropeaspthrvalArgArgmetmet 240
Db 791 ACGGCGGTGGCCGGGCTGTGTCTTACCCCTTCGACGCGGCGGCGCATGATGATG 850
Qy 241 GlnserglyArgglyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArglys 260
Db 851 CAGTCCGGGGCGAAAGAGGCTGACATGTCACAGGGGACCGTGCAGCTGTGGAGGAG 910
Qy 261 llephearasppluglyglylysAlaphepelysglyAlaTrpSeranValleuarg 280
Db 911 ATCTTCAGAGATGAGGGGGGCGAAGGCTTCTCAAGGGGTGCGTCCAAAGCTCCTGCGG 970
Qy 281 GlyMetGlyGlyAlaPheValleuValleuTyrAspGluLeuLysValle 298
Db 971 GGCATGGGGGGCGCTTGTGTGTCTTGTGCTGACGAGAGCTCAAGAGGTGATC 1024

RESULT 3
US-09-434-354-2
; Sequence 2, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelebi, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-434-354-2

Alignment Scores:
Pred. No.: 7,39e-169 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
Gaps: 0
DB: 4

US-09-811-094-33 (1-298) x US-09-434-354-2 (1-897)

Qy 1 MetrhngluglnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaAla 20
Db 1 ATGACAGATGCCGATTTGCTTCGCAAGAGACTTCTGCGAGGTGAGATGGCGCGAGCC 60
Qy 21 lIeserlysthrAlaValAlaProIleGluArgValLysLeuLeuLeuGlnValGlnHis 40
Db 61 ATCTCCAGAGACGCGGTGACCGCCATCGAGCGGTCACAGCTGCTGTCGACGTGACAGAT 120
Qy 41 AlaserlysglnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
Db 121 GCCACGACGACATCTGCTGACATATGACATACAAAGGCAATATGACTGCGTGGTCCGT 180

Qy 61 lleProLysGluGlnGlyValleuSerPheTrpArgGlyAsnLeuAlaAsnValIlearg 80
Db 181 ATTCACAGAGACAGAGAAATCTGTCTTCTGCGCGGATACCTGGCCAAATCATCANAA 240
Qy 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCGACCCAGGCTCTTAACCTGCGCTTCAAGATTAATACAAAGCATCTTCCG 300
Qy 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGTGTGTGACACAGAGAACCCAGTTTGGCTTACTTGTGACAGGATTTGGCATCGGGT 360
Qy 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGTGGCGCGAGGGGCGACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTAGCAGCTGATGTGGTAAAGCTGAGCTGAAGGCAATTCGAGGCTCGGTGACTGC 480
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
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Db 601 ATGCTTCGCGATCCCAAGAACACTCACATCGCATGCTGATGCCACAGACTGTC 660
Qy 221 ThrAlaValAlaGlyValValSerTyrPropeaspthrValArgArgmetmet 240
Db 661 ACTGCTGTGGCGGGGTGACTTCTTATCCATTTGACACCGTTCGCGCGCATGATGATG 720
Qy 241 GlnserglyArgglyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArglys 260
Db 721 CAGTACGGGCGCAAGAGACTGACATCATGTCACAGGACCGTTCAGCTGTGCGGAGG 780
Qy 261 llephearasppluglyglylysAlaphepelysglyAlaTrpSeranValleuarg 280
Db 781 ATTCCTCTGATGAGAGAGGCAAGCTTTTTCACAGGTCGATGCTCAATGTTCACAGA 840
Qy 281 GlyMetGlyGlyAlaPheValleuValleuTyrAspGluLeuLysValle 296
Db 841 GGCATGGGGGGCGCTTGT 888

RESULT 4
US-08-961-871-9
; Sequence 9, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Graham, Brett H.
; APPLICANT: Macgregor, Grant R.
; TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
; TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
; STREET: 5370 Manhattan Circle, Suite 201
; CITY: Boulder
; STATE: Colorado
; COUNTRY: US
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

US-08-961-871-11

Alignment Scores:

Pred. No.:	1.24e-162	Length:	1259
Score:	1405.00	Matches:	263
Percent Similarity:	94.30%	Conservative:	18
Best Local Similarity:	88.26%	Mismatches:	17
Query Match:	91.06%	Indels:	0
DB:	3	Gaps:	0

US-09-811-094-33 (1-298) x US-08-961-871-11 (1-1259)

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OY 21 IleserLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHs 40
DB 250 GTCTCCAAAGCGCGGTGCGCCGATCGAGAGGATCAACACTGCTGCGAGGTCAGCAT 309
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnIleValAlaPcysIleValArg 60
DB 310 GCCAGCAAAAGATGAGGAGAGAGAGAGAGATCAAGCATGATGATGTCGTGAGCA 369
OY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
DB 370 ATCCCAAGAGAGAGAGGCTTCTCTCTCTGAGAGGATACCTGGCAACGTGATCCG 429
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 430 TACTTCCCACTCAAGCCCTGAACCTGCTTCAAGACAACTACAAAGCATGATGATCCG 489
OY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 490 GGAGGCGTGGATCGCATTAAGAGATGTCGGCTACTTGGCTGATACCTGGCGCTGCT 549
OY 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
DB 550 GGGGAGCTGGGCGCACCTCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 609
OY 141 LeuAlaAlaAspValAlaGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 610 CTGGCTGCGAGCTGGGCGAGGAGATCTCCAGCAAGATTAAGGGTGGGCGCATCT 669
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 670 CTCACCAAGATCTTCAAGTCGAGCGGCGTGGGCTCTACAGGCTTTCAGTCTCT 729
OY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 730 GTCCAGGCGCATCATCATCTACAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 789
OY 201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
DB 790 ATGCTGCCAGACCCCAAGAGATGTGCATATCTGAGCTGATGATGATGCCAGAGTGG 849
OY 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgIleMetIle 240
DB 850 ACAAGCGTGGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 909
OY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
DB 910 CAGTGTGCGCGCAAAAGGGGCTGATATTATGATACAGGGGAGCACTGACCTGAGAGAG 969
OY 261 IlePheArgAspGluGlyGlyLysAlaPhePheLysGlyAlaTrpSerTrpValLeuArg 280
DB 970 ATTGCAAAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1029
OY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 1030 GGCATGCGGTGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083

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RESULT 6

US-09-434-354-1

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; Sequence 1, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Velicelbi, Gonul
; APPLICANT: Davis, Robert E.

```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; CURRENT APPLICATION NUMBER: US/09/434,354
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Homo sapien

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US-09-434-354-1

Alignment Scores:

Pred. No.:	1.84e-160	Length:	894
Score:	1385.50	Matches:	260
Percent Similarity:	94.30%	Conservative:	21
Best Local Similarity:	87.25%	Mismatches:	16
Query Match:	89.79%	Indels:	1
DB:	4	Gaps:	1

US-09-811-094-33 (1-298) x US-09-434-354-1 (1-894)

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OY 1 MethrGlUGlnAlaIleSerPheAlaIysAspPheLeuAlaGlyIleAlaAla 20
DB 1 ATGGGGGATCAGCTTGAAGCTTCTTAAGAGCACTTGGGAGGATCCGCCGCC 60
OY 21 IleserLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHs 40
DB 61 GTCTCCAAAGCGCGGTGCGCCGATCGAGAGGATCAACACTGCTGCGAGGTCAGCAT 120
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnIleValAlaPcysIleValArg 60
DB 121 GCCAGCAAAAGATGAGGAGAGAGAGAGAGATCAAGCATGATGATGTCGTGAGCA 180
OY 61 IleProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
DB 181 ATCCCAAGAGAGAGGCTTCTCTCTCTGAGAGGATACCTGGCAACGTGATCCG 240
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 241 TACTTCCCACTCAAGCCCTGAACCTGCTTCAAGACAACTACAAAGCATGATGATCCG 300
OY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 301 GGGGCGTGGAGCGGATTAAGAGATGTCGGCTACTTGGCTGATACCTGGCGTCCGT 360
OY 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGGGCGGCGGCGCACCTCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
OY 141 LeuAlaAlaAspValAlaGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 421 TTGGCTGCTGATGTTGGGCGAGCGC--GCCAGCGGATGATCCATGCTGGCGATCTGT 477
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
DB 478 ATCATCAAGATCTTCAAGCTGATGAGCGCGAGGCGCTTACAGGCTTTCACAGCTCT 537
OY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200

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Thu Aug 28 08:34:56 2003

us-09-811-094-33.p2n.inl

Page 6

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Db      538  GTCCAGGATCATATATAGAGCTGCTTCCGAGCTATGATATGATCCAGGCG 597
QY      201  MetLeuProAspProIysAsnThrHisIleValAlaSerTrpMetIleAlaGlnThrVal 220
Db      598  ATGCGCGCTGACCCCAAGAACGTCACATTTTGTGAGCGTGATGATCCAGAGTGTG 657
QY      221  ThrAlaValAlaGlyAlaValSerTrpProAspThrValAlaArgTrgArgMetMet 240
Db      658  ACGGAGCGGAGGCGCTGCTGCTACCCCTTGCACCTGCTGCTGATGATGATG 717
QY      241  GlnSerGlyArgGlyGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgLys 260
Db      718  CAGTCGCGCGGAGGAGGCGGATATATGATACAGGCGGACAGTGTGCTGAGGAGAG 777
QY      261  IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
Db      778  ATTGCAGAAAGACGAGAGGAGCCAGGCGCTTTCAGAAAGCGCTGCTCAGATGCTGAG 837
QY      281  GlyMetGlyGlyAlaPheValAlaValLeuValLeuTrpAspGluLeuLysValIle 298
Db      838  GGCATGGCGCGCTGCTTGTATGCTGATGATGATGATGATGATGATGATGATG 891

RESULT 7
US-09-996-243-288
: Sequence 288, Application US/09996243
: Patent No. 6478825
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferreira, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerltzen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C13
: CURRENT FILING DATE: 2001-11-13
: PRIOR APPLICATION NUMBER: US/09/996,243
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600

: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: PRIOR APPLICATION NUMBER: 60/087607
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087609
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087759
: PRIOR FILING DATE: 1998-06-02
: PRIOR APPLICATION NUMBER: 60/087827
: PRIOR FILING DATE: 1998-06-03
: PRIOR APPLICATION NUMBER: 60/088021
: PRIOR FILING DATE: 1998-06-04
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: PRIOR FILING DATE: 1998-06-04
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: PRIOR FILING DATE: 1998-06-04
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: PRIOR FILING DATE: 1998-06-04
: PRIOR APPLICATION NUMBER: 60/088030
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: PRIOR FILING DATE: 1998-06-04
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: PRIOR APPLICATION NUMBER: 60/088876
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: PRIOR APPLICATION NUMBER: 60/089105
: PRIOR FILING DATE: 1998-06-12
: PRIOR APPLICATION NUMBER: 60/089440
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089512
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089514
: PRIOR FILING DATE: 1998-06-16
: PRIOR APPLICATION NUMBER: 60/089532
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089538
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089598
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089599
: PRIOR FILING DATE: 1998-06-17
: PRIOR APPLICATION NUMBER: 60/089600
: PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090435
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090444
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090445
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090535
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090540
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090542
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090676
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090678
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090690
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090694
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090695
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Alignment Scores:

Pred. No.:	2,98e-28	Length:	3334
Score:	314.00	Matches:	92
Percent Similarity:	50.68%	Conservative:	58
Best Local Similarity:	31.08%	Mismatches:	115
Query Match:	20.35%	Indels:	32
DB:	4	Gaps:	10

US-09-811-094-33 (1-298) x US-09-996-243-288 (1-3334)

QY 10 LysAspPheLeuAlaGlyIleAlaAlaIleSerIysThrAlaValAlaProIle 29
DB 622 AGACACCTGGTGGCAGAGGTGGGCGGCGTATCCAGAACCTGCACGCGCCCTG 681
QY 30 GluArgValIysLeuLeuGlnValGlnHisAlaSerIysGlnIleAlaAlaPlys 49
DB 682 GACAGGCTCAGGTGCTCATGAGTCC---CATGCTCCGC-----AGC 723
QY 50 GlnTyrIysGlyIleValAlaPysIleValArgIleProIysGlnGlnIysAlaLeuSer 69
DB 724 AACACATGGGCGATGCTGTGGCTTCACTCATGATGATTCGAGAGAGGCGCCAGTCA 783
QY 70 PheTyrArgIysLeuAlaSerValIleArgTyrPheProThrGlnAlaLeuAlaPhe 89
DB 784 CTCTGGCGGGGCATGACATCAACGTCCTCAAAATGCCCCCAATCAGCCATCAATTC 843
QY 90 AlaPheIysAspIysTyrIysGlnIlePheLeuGlyIleValAlaPlysHisThrGlnPhe 109
DB 844 ATGGCCATGACAGATCAAGCC-----CTGTGTGTTGATGATCCAGAGACT----- 891
QY 110 TrpArgTyrPheAlaGlyAlaLeuAlaSerGlyIleAlaAlaIleAlaIleThrSerLeuCys 129
DB 892 ---CTGAGATTCACGAGAGGCTTGTGGCGGCTTGGCAGGGCCATCGCCAGAGC 948
QY 130 PheValTyrProIysAspPheAlaArgTyrArgLeuAlaAlaPysValGlyIysSerGly 149
DB 949 AGCATCTACCCATGAGAGTCTGTAAGACCGGATGCG-----CTGCGGAAGACAGGC 1002
QY 150 ThrGluArgIysLeuArgIysLeuGlyAlaPysCysLeuValIysIleThrIysSerArgIys 169
DB 1003 -----CAGTACTCAGGAATGCTGATGCGCCAGAGATCTCGCCAGAGAGGG 1053
QY 170 IleArgGlyLeuTyrGlnIysPheSerValSerValGlnIysIleIleIleTyrArgAla 189
DB 1054 GTGGCGCCTTCTACAAAGCTATGTCCTCCACATGCTGGGATCATCCCTATGCCGGC 1113
QY 190 AlaTyrPheGlyValTyrAspThrAlaIysGlyMet----- 201
DB 1114 ATCGACCTTCAGCTACGAGAGCGCTCAACATGCCGCTGCAGACATGACGTGAC 1173
QY 202 LeuProAspProIysAsnThrHisIleValAla---SerTrpMetIleAlaGlnThrValTh 221
DB 1174 AGCGCGGACCC-----GGCGTGTGTGCTCTGCGCTGTGACACCATGTCCAGT 1224
QY 221 AlaValAlaGlyValAlaValSerTyrProPheAspThrValArgArgMetMetG1 241
DB 1225 ACCTGTGGCCAG---CTGGCCAGAGTACCCCGCGCTGTGACAGACCGGATGACAGGGCA 1283
QY 241 nserGlyArgIysGlyAlaPysIleMetTyrThrGlyThValAlaPysCysTrpArgIysI1 261
DB 1284 AGCCTATATGAGAGCGCTCCGAGGAGACCATGAGACGCTC-----TTCAAAACATAT 1337
QY 261 ePheArgAspGluGlyValIysAlaPhePheIysGlyAlaIleTrpSerAsnValLeuValG1 281
DB 1338 CTGTGGAGCCGAGAGGGGCTTGGGCGCTGTACAGGGGCTGGCCCACTTCTATGAAGGT 1397
QY 281 yMetGlyIleAlaPheVal---LeuValLeuTyrAspGluLeuIys 295

[illegible]

```

Db      1115  AATGACCTAGCTGTCTATGACACATTG-----ValValSerTyrMetIleAlaGln 1153
Oy      210  Ile-----ValValSerTyrMetIleAlaGln 218
Db      1154  CTCACGGCTACCGACTAAACAGTCAGACCCCGGGGTTCGTCGCTCCGCGCTGTGCT 1213
Oy      219  ThrValThrAlaValAlaGly---ValValSerTyrProPheAspThrValAlaGlnGly 237
Db      1214  ACTATCTCCAGTACTCTTGTCGGCAGCTGCGACGTACCCAGCTACAGCCCTGCTGACAGCCGG 1273
Oy      238  MetMetMetIleSerGlyAlaGlyAlaAspIleMetTyrThrGlyThrValAspGly 257
Db      1274  ATGAGGACCAACCCCTCCACTTGTAGGGGCGACCTGAGAlaPheMetGlyAlaTTPSerAsn 1327
Oy      258  TyrAlaGlyIlePheAspGlyAlaGlyAlaAlaPheMetGlyAlaTTPSerAsn 277
Db      1328  TTCAAACAGATTCTCGCGACTGAGGGGCGCTTTGGCTCTACCGGGGGCTGGCCCCAAC 1387
Oy      278  ValLeuValGlyMetGlyAlaPheVal---LeuValLeuTyrAspGluLeuGly 295
Db      1388  TTCATGAGAGTGATCCCGGCTGTGAGCATCAGCTACGTAGTGTCTACGAAACCTGTAAG 1444

RESULT 9
US-09-312-283C-262
Sequence 262, Application US/09312283C
Patent No 6573095
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated from Skin Cells
FILE REFERENCE: 11000.1011c2
CURRENT APPLICATION NUMBER: US/09/312,283C
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 425
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 262
LENGTH: 1816
TYPE: DNA
ORGANISM: Mouse
US-09-312-283C-262

Alignment Scores:
pred. No.: 2,82e-28 Length: 1816
Score: 311.00 Matches: 88
Percent Similarity: 50.17% Conservative: 62
Best Local Similarity: 29.43% Mismatches: 111
Query Match: 20.16% Indels: 38
Db: 4 Gaps: 11

US-09-811-094-33 (1-298) x US-09-312-283C-262 (1-1816)
Oy      10  LysAspPheLeuAlaGlyIleAlaAlaAlaIleSerYsThrAlaValAlaProIle 29
Db      623  AGGCACCTGCTGGCGACGAGTGGGGGAGGGCGAGTTTCCAAACCTGCACTGCCCCCTG 682
Oy      30  GluAlaValIleLeuLeuGlnValGlnIleAlaSerIysGlnIleAlaAlaAspLys 49
Db      683  GACGAGCTAAGTCTCATCAGAGTC---CATGGCTCCGCC-----AGC 724
Oy      50  GluTyrIleGlyIleLeuAlaAspCysIleValAlaGlyIleProIysGlnGlnIleValLeuSer 69
Db      725  AACAACATGTGATCTGTGAGTTCACACAGATGATTCAGCAAGAGGGGAGCCCAAGTCA 784
Oy      70  PheTyrPheGlyAspLeuAlaAsnValIleAspGlyrPheProThrGlnAlaLeuAsnPhe 89
Db      785  CTCTGGGGGGGCAACGCCATCAATATCTCTCAAAATTTGGCCCTGAGTCGGGCACTCAATTC 844

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QY 90 AlaPheLysAspLysTyrLysGlnIlePheLeuGlyGlyValAspLysHisThrGlnPhe 109
 Db 845 ATGGCATATAGCAGATGAACGG-----CTTGTGCGTAGTCAGACAGAGC----- 892
 QY 110 TPTATGTYRPhaAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGlyAlaThrSerLeuGly 129
 Db 893 ---CTGAGATATCCAGAAAGGCTTGTGGAGGCTCTTGGCCGAGCATTGCCAGAGT 949
 QY 130 PheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAspValGlyLysSerGly 149
 Db 950 AGCATCTACCAATGAGAGGTCTGAAAGACCCGAAATGCC-----CTGGGAAACAGCA 1003
 QY 150 ThrGlnArgGlnPheArgGlyLeuGlyAspCysLeuValLysIleThrLysSerAspGly 169
 Db 1004 -----CAGTACTCCGCGCATGTGAGCTGTGCCAGAGATCTTGGCTAAAGAGCT 1054
 QY 170 IleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIleIleIleTyrArgAla 189
 Db 1055 GTAGCTGCTTCTTACAAAGGCTACATCCCAACATCTGTGGGATCATCCCTATGCTGGC 1114
 QY 190 AlaTyrPheGlyValTyrAspThrAlaLysGlyMetLeuProAspProLysAsnThrHis 209
 Db 1115 ATCGACCTAGCTGTCTATGACATATG-----AAATATACCTGG 1153
 QY 210 Ile-----ValValSerTrpMetIleAlaGln 218
 Db 1154 CTCACGCGCTACGACGTAACAGTCAGACGCCGCGGTGTGCTGCTGCTGCTGCTGCT 1213
 QY 219 ThrValThrAlaValAlaGly---ValValSerTyrProPheAspThrValArgArg 237
 Db 1214 ACTATCTCCAGTACTTGTGGCCAGCTGCGCAGCTACCCAGCTGAGCCCTGTGTCAGACCCG 1273
 QY 238 MetMetMetGlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCys 257
 Db 1274 ATCGAGGACACAAAGCCCTCATTGAGGCGCAGACCTGAGTAACCATGACGAGCCCTC 1327
 QY 258 TrpArgLysIlePheArgAspGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsn 277
 Db 1328 TTCAAACACATCTCTGCGGACTGAGGGGCGCTTGGCTTACCGGCGGCGGCCCCCAAC 1387
 QY 278 ValLeuArgGlyMetGlyGlyAlaPheVal---LeuValLeuTyrAspGluLeuLys 295
 Db 1388 TTCATGATAGGTATTCGCCGCTGTGAGCATACGCTACGTGTGTCAGAAACCTGGAAG 1444
 RESULT 10
 US-09-620-312D-283
 : Sequence 283, Application US/09620312D
 : Patent No. 6569662
 : GENERAL INFORMATION:
 : APPLICANT: Tang, Y. Tom
 : APPLICANT: Liu, Chenghua
 : APPLICANT: Asundi, Vinod
 : APPLICANT: Zhang, Jie
 : APPLICANT: Ren, Feiyang
 : APPLICANT: Chen, Rui-hong
 : APPLICANT: Zhao, Qing A.
 : APPLICANT: Wehrman, Tom
 : APPLICANT: Xue, Aifong J.
 : APPLICANT: Yang, Yonghong
 : APPLICANT: Wang, Jian-Rui
 : APPLICANT: Zhou, Ping
 : APPLICANT: Ma, Yungang
 : APPLICANT: Wang, Dunrui
 : APPLICANT: Wang, Zhiwei
 : APPLICANT: John Tillinbost
 : APPLICANT: Drmanac, Radoje T.
 : TITLE OF INVENTION: No. 6569662el Nucleic Acids and
 : FILE REFERENCE: Polypeptides
 : CURRENT APPLICATION NUMBER: US/09/620,312D
 : CURRENT FILING DATE: 2000-07-19
 : PRIOR APPLICATION NUMBER: 09/552,317
 : PRIOR FILING DATE: 2000-04-25

: PRIOR APPLICATION NUMBER: 09/488,725
 : PRIOR FILING DATE: 2000-01-21
 : NUMBER OF SEQ ID NOS: 1105
 : SOFTWARE: PL_FL_genes Version 1.0
 : SEQ ID NO 283
 : LENGTH: 2663
 : TYPE: DNA
 : ORGANISM: Homo sapiens
 : FEATURE:
 : NAME/KEY: CDS
 : LOCATION: (115)..(2157)
 US-09-620-312D-283
 Alignment Scores:
 Pred. No.: 1,28e-26 Length: 2663
 Score: 299.50 Matches: 88
 Percent Similarity: 44.85% Conservative: 47
 Best Local Similarity: 29.24% Mismatches: 139
 Query Match: 19,41% Indels: 27
 Gaps: 9
 US-09-811-094-33 (1-298) x US-09-620-312D-283 (1-2663)
 QY 4 GlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAlaIleSerLys 23
 Db 1084 CAGATTGCCAGCTCTCTTACAGATTCACCTGTGGCTAGTCTGAGCTGTGGAGCC 1143
 QY 24 ThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHisAlaSerLys 43
 Db 1144 ACTGACGTGATCTTATAGATCTGTGGAAGACCCGAAATGCAAAACAGGCTGCTGGC 1203
 QY 44 GlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArgIleProLys 63
 Db 1204 TCGTGTGTGGGAGCTAATGTACAAACACGCTTGACGTGTTTAAAGAAAGCTTGGCT 1263
 QY 64 GluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyrPhePro 83
 Db 1264 TATGAGGCGCTCTTGTGACTCTACAGGGGCTGTATACACACTTATAGGGGTGGCTCCA 1323
 QY 84 ThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 Db 1324 GAAAGGCCATTAATACGACTGTTAATGATTTGTTGGGCAAAATTTACCAAGAGAT 1383
 QY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
 Db 1384 GGCTCGTGTCCA-----CTTCACACAGAGTCTTGGCTGCA 1419
 QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 Db 1420 GGCTGTGCTGAGGCTCTCAGTCATTTCACCAACCATTTGAGATAGTGAAGATTGCT 1479
 QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGlnArgGlnPheArgGlyAspCys 160
 Db 1480 CTCGACGTA---GCTGAGAGATCACCCGAGCCAGACTGACGCCCTG----- 1527
 QY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSer 180
 Db 1528 -----AAGTGTCTCCGGAGCTTGGGAATTTTGTCTGTATAGAGGTGCCAAGCTGT 1581
 QY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 Db 1582 TTCCTCCGAGACATTCCTCTGCAATCTATTTCTTATGCTCATTCGCAAACTA 1641
 QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
 Db 1642 CTTCGTGCTGAT---GAAATGACACAGTGGAGGTTTAAATCTTCTGCA-----GCT 1692
 QY 221 ThrAlaValAlaGlyVal-----ValSerTyrProPheAspThrValArgArg 236
 Db 1693 GAGCGCATGTCAGAGTGTCCAGCTGCATCTGTGTGACCCCTGTATGTCATCAAGACA 1752
 QY 237 ArgMetMetMetGlnSerGlyArgGlyAlaAspIleMetTyrThrGlyThrValAsp 256
 Db 1752


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Db      560 GGCACCATTAATAATGGGATTACCAAGCTTGACCCCTTATTCGTACAGCTTTAGAA 619
QY      105 LysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGly 124
Db      620 GATGAACCT-----CCTTAATTAATATGATCGTGGGGTAGTGCAGGA 664
QY      125 AlaThrSerLeuGlyCysPheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAsp 144
Db      665 GTGATTCCTTCACACTATACCAATCCACCGATGTTCTAAGATTCGAATGCAGGCT--- 721
QY      145 ValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspGlyAspGlyLeuValLysIle 164
Db      722 -----CAAGGAAGCTTTGTTCCAGAGGACATGATGGAAAGC---TTTATCGAATATA 769
QY      165 ThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIle 184
Db      770 TACCAACAGAAAGACACCAAGGGCTGTGTGAGGGGTGTGGTTCACACTGCTCAGCGCT 829
QY      185 IleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLys----- 199
Db      830 GCCATGCTGTAGAGTAGAGCTACACAGCTATGATGATTAATTAAGAGCATTTAATATTG 889
QY      200 ---GlyMetLeuProAspProLysAsnThrHisIleValSerThrMetIleAlaGln 218
Db      890 TCGAGATATGATGGCGCATACATTTTAACCTGCTGTTCCAGCTTT----- 937
QY      219 ThrValThrAlaValAlaGlyValIleSerTyrProPheAspThrValAlaArgArgMet 238
Db      938 ACATGTGTGTGGCTGGGGCTGTGGCTCAACCGGTTGATGTGGTGAACCTCGCATG 997
QY      239 MetMetGlnSerGlyTyrGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTrp 258
Db      998 ATGAACCAAGAGGCAATCGTGGAGCATGTGATCTCTAATAAGGCACTGTGTATGTGATT 1057
QY      259 ArgLysIlePheArgAspGlnGlyGlyLysAlaPhePheLeuValIleTyrPheSerAsnVal 278
Db      1058 TTTAAAGATGTGAAACATGAGGCTTTTTCACCTATTAAGGATTTTGGCCAAACTGG 1117
QY      279 LeuArg---GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysVal 297
Db      1118 CTTCGGCTTGACCCCTGGAACATCATTTTATTATACATACGAGCAGCTAAAGAGGCTT 1177

RESULT 13
US-09-501-558-1
; Sequence 1, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; FILE REFERENCE: Lex-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 876
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-501-558-1

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Alignment Scores:

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Pred. No.:      2 24e-25      Length:      876
Score:          283.50      Matches:      87
Percent Similarity: 46.84%      Conservative: 54
Best Local Similarity: 28.90%      Mismatches: 129
Query Match:     18.37%      Indels: 31
DB:              4          Gaps: 9

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US-09-811-094-33 (1-298) x US-09-501-558-1 (1-876)

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QY      10 LysAspPheLeuAlaGlyGlyIleAlaAlaAlaIleSerLysThrAlaValAlaProIle 29
Db      19 AAGCCGTTGTGTACGGGGGGCTGGCTTCATACAGCTAGAGCGGTACATTTCCAAATT 78
QY      30 GluArgValLysLeuLeuGlnValGlnHisAlaSer-----LysGln 44
Db      79 GATTTAACCAAGACAGCGGCTCCAGATTCAGAGCCAGACGAATGATGCAGAAATTTAAGAA 138
QY      45 IleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArgIleProLysGlu 64
Db      139 ATT-----AGATACGAGGAATGTTCACGCACTTATGATGAGATAGGACAGAA 186
QY      65 GlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaAsnValIleArgTyrPheProThr 84
Db      187 GAAGGGGTGAAGACACTACTACGCGGGATTTGCCCGCGATGTTAGCCAGCATCCTAT 246
QY      85 GluAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeuGlyGlyValAsp 104
Db      247 GGCACCATCAAGATAGGCACTTACACAGCTTGAGAGCACTATTCATGAAACGCCAGAA 306
QY      105 LysHisThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGlyGlyAlaAlaGly 124
Db      307 GATGAACCT-----CTACCGATTAATGTGATGATGGAATTCGTCTGGA 351
QY      125 AlaThrSerLeuGlyCysPheValTyrProLeuAspPheAlaArgThrArgLeuAlaAlaAsp 144
Db      352 GTCATATCTTCACACCATGCTATACCAACGATGTTTGAATAATTCGAGATGCAAGCG--- 408
QY      145 ValGlyLysSerGlyThrGlnArgGlnPheArgGlyLeuGlyAspCysLeuValLysIle 164
Db      409 -----CAAGCAACACCAATTCAA-----GGAAGATGTATAGCAACTTCAGCAACATT 456
QY      165 ThrLysSerAspGlyIleArgGlyLeuTyrGlnGlyPheSerValSerValGlnGlyIle 184
Db      457 TACCAAGACAGAGGAGACAGACAGCTGTGAAAGGTGTCTCCCTTACTGCGCAGAGGCT 516
QY      185 IleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLys----- 199
Db      517 GCTATGCTGTGTGTGTGAGAGCTGCCGCTATGACATACCAAGAAAGCATCTTATTC 576
QY      200 ---GlyMetLeuProAspProLysAsnThrHisIleValSerThrMetIleAlaGln 218
Db      577 TCAAGCTGATGTGAGAGCACTGTGTATATCCACTTCCTCAAGCTTC----- 624
QY      219 ThrValThrAlaValAlaGlyValIleSerTyrProPheAspThrValAlaArgArgMet 238
Db      625 ACCGTGTGTGTGGCAGGGGCCCTGGCTCAAAACCTGTGTATGTGTGAGGACACGTAATG 684
QY      239 MetMetGlnSerGly---ArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCys 257
Db      685 ATGAATACAGAGAGTGTGAGATGAGCATGTTTGGCTACACAGGAAACCTCGAGATTGC 744
QY      258 TrpArgLysIlePheArgAspGlnGlyGlyLysAlaPhePheLysGlyAlaTrpSerAsn 277
Db      745 TTGTATACAGACATGAAGATGAAGGCTTTTCTCTCTATTAAGGCTTTTGCCCAAT 804
QY      278 ValLeuArg---GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGlnLeuLysVal 296
Db      805 TGTGTGAGACTTGCTCTTGGAATATCATTTTCTTTGTGACATACGACGCTTGAGAGAA 864
QY      297 Val 297
Db      865 TTG 867

RESULT 14
US-09-160-119-3
; Sequence 3, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: SOUCHET, STEPHANE
; APPLICANT: SOUCHET, MICHEL
; APPLICANT: BRILL, ANTOINE

```



```
Db 1373 GGCTGGCTGGAGGCTCCAGGTGATTTCACAAATCCTTTAGAAATCGTCAAGATCCGT 1432
Qy 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 1433 TTGCAAGTG---GCAGAGAAATTCACCACTGGTCCGAGTCAGTCTCTG----- 1480
Qy 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuTyrginglyPheSerValSer 180
Db 1481 -----TCGTGCTGCGGGACCTGGGGTTTGGGATCTACAAAGGTGCCAAAGCATGC 1534
Qy 181 ValGinglyIleIleIleThrArgAlaIleTyrginglyValTyraSprThrAlaLysGly 200
Db 1535 TTCTGCGGGACATTCCTTTCGCGCCATCTTCCGTCTATGCTCATGTGAAGCT 1594
Qy 201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
Db 1595 TCCTTTGCAAAATGAAGATGGGAGGATTACCCAGAGAGCCCTGCTCTTACCTGGTGCATTA 1654
Qy 221 ThrAlaVal---AlaGlyValIleSerTyroPheAspThrValArgArgMetMet 239
Db 1655 GCTGGTATGCTGCAGACATCTTGTAGACCCCTGCTGATGTTATCAAGACGAGA----- 1708
Qy 240 MetGlnSerGlyArgLysGlyAlaAspIleMetTyroThrGlyThrValAspCysTrpArg 259
Db 1709 TTACAGGTGGCTGCCCGGCTGGCCCAACCACTTACAGCGAGTGAAGACTGCTTTAGA 1768
Qy 260 LysIlePheArgAspGlyLysIleLysAlaPhePheLysGlyAlaTrpSerAsnValLeu 279
Db 1769 AAGATTACTGCTGGAAGAACCAAGCTCTGTGGAAGGACCTGCTGCTGTATTT 1828
Qy 280 ArgGlyMetGlyGlyAlaPheValLeuValLeuTyraSprGluLeu 294
Db 1829 CGATCCTCACCCAGTTTGTGTAACTTGTGACTTACGAATTTG 1873
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Search completed: August 27, 2003, 14:23:53
Job time : 96 secs

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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August.27, 2003, 13:44:11 ; Search time 330 Seconds

(without alignments)
2071.778 Million cell updates/sec

Title: US-09-811-094-33

Perfect score: 1543
Sequence: 1 MTEGASIFAKDFLAGGIAA.....LRGAGAFVLYVELKVI 298

Scoring table:

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Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 1533700 seqs, 1147125425 residues

Total number of hits satisfying chosen parameters: 3067400

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-IOOCL=0 -IOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blsum62
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Database: Published Applications.NA.*

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16: /cgn2.6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
17: /cgn2.6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match length	ID	Description
1	1543	100.0	897 9	US-09-811-094-33 Sequence 3, Appl1

2	1543	100.0	897 9	US-09-810-644-3	Sequence 3, Appl1
3	1543	100.0	897 10	US-09-185-904A-3	Sequence 3, Appl1
4	1543	100.0	1212 10	US-10-037-270-687	Sequence 687, Appl1
5	1510	97.9	2592 13	US-10-044-090-152	Sequence 152, Appl
6	1454	94.2	897 9	US-09-811-094-2	Sequence 2, Appl1
7	1454	94.2	897 9	US-09-810-644-2	Sequence 2, Appl1
8	1454	94.2	897 10	US-09-185-904A-2	Sequence 2, Appl1
9	1424	92.3	1196 10	US-09-917-800A-1327	Sequence 1327, Appl
10	1409	91.3	1711 14	US-10-198-846-13437	Sequence 13437, A
11	1385.5	89.8	894 9	US-09-811-094-1	Sequence 1, Appl1
12	1385.5	89.8	894 10	US-09-810-644-1	Sequence 1, Appl1
13	1385.5	89.8	894 10	US-09-185-904A-1	Sequence 1, Appl1
14	1356.5	87.9	1116 10	US-09-968-708-213	Sequence 213, Appl
15	1356.5	87.9	1116 10	US-09-880-107-2096	Sequence 2096, Appl
16	1356.5	87.9	1116 14	US-10-171-581-48	Sequence 48, Appl
17	1193	77.3 <td>2706 14</td> <td>US-10-103-313-611</td> <td>Sequence 611, Appl</td>	2706 14	US-10-103-313-611	Sequence 611, Appl
18	936	60.7	720 9	US-09-910-943-105	Sequence 105, Appl
19	760.5	49.3	957 10	US-09-801-368-251	Sequence 251, Appl
20	750.5	48.6	1158 10	US-09-938-842A-608	Sequence 608, Appl
21	750	48.6	468 11	US-09-918-995-26014	Sequence 26014, A
22	749.5	48.6	1536 9	US-09-734-569-169	Sequence 169, Appl
23	742.5	48.1	1493 9	US-09-770-445-7	Sequence 7, Appl1
24	737	47.8	927 14	US-10-128-714-2338	Sequence 2338, Appl
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26	734.5	47.6	1458 12	US-10-141-478A-1	Sequence 1, Appl1
27	708	45.9	501 9	US-09-833-790-161	Sequence 161, Appl
28	700	45.4	493 11	US-09-918-995-9153	Sequence 9153, Appl
29	698.5	45.3	2037 12	US-10-259-165-191	Sequence 191, Appl
30	683	44.3	858 14	US-10-198-846-0464	Sequence 9464, Appl
31	679	44.0	1186 14	US-10-128-714-1338	Sequence 1338, Appl
32	679	44.0	1186 14	US-10-128-714-5338	Sequence 5338, Appl
33	679	44.0	3185 14	US-10-128-714-5338	Sequence 5338, Appl
34	679	44.0	3186 14	US-10-128-714-5338	Sequence 5338, Appl
35	670	43.4	410 11	US-09-918-995-16539	Sequence 16539, A
36	658	42.6	417 11	US-09-918-995-1864	Sequence 1864, Appl
37	656	42.5	483 11	US-09-918-995-1495	Sequence 1495, Appl
38	649.5	42.1	464 9	US-09-864-761-1408	Sequence 1408, Appl
39	646	41.9	513 11	US-09-918-995-37948	Sequence 37948, A
40	640	41.5	485 11	US-09-918-995-8792	Sequence 8792, Appl
41	607	39.3	474 11	US-09-918-995-6148	Sequence 6148, Appl
42	607	39.3	484 11	US-09-918-995-6070	Sequence 6070, Appl
43	606	39.3	460 11	US-09-918-995-1700	Sequence 1700, Appl
44	594	38.5	434 10	US-09-960-352-12424	Sequence 12424, A
45	568	36.8	420 11	US-09-918-995-5524	Sequence 5524, Appl

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 3, Application US/09811094
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pel, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien

Thu Aug 28 08:34:56 2003

us-09-811-094-33.p2n.rnpb

Page 2

US-09-811-094-3	
Alignment Scores:	
Pred. No.:	2,32e-200
Score:	1543.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
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	Length: 897
	Matches: 298
	Matched: 0
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Db	1	ATGAGGAAAGGGCAATCTCTCTGGCCAAAGACTTCTGGCCGAGGACATGGCCGCC	60
QY	21	IieserlystrhalavalalaapolliegtuarvallylsleuleuenglnValGHis	40
Db	61	ATCTCCAGAGCGGGCGGGCTCGCATCCAGCGGGGCAAGCTGGCTGGAGGTCCAGAC	120
QY	41	AlaserlysglnIlealalaasplysglnlyrlysglylleValAspcysilleValArg	60
Db	121	GGCAGAGAGCAAGATCGCGCGCCGACAAAGCTCAAGGGCAATCGAGACGTCTTCGC	180
QY	61	IleProLySGuIngInglyValIleuserPheTrparGlysanleuAlaasnValIleArg	80
Db	181	ATCCCCAAGAGACAGGGCGTGTCTCTCTTGAGGGGCAACCTTGCCAACCTCAATTGC	240
QY	81	TyrPheProthGlnAlaIleuAnPhealAapheLyAsApLyTYrLYrsglnIlePheLeu	100
Db	241	TACTTCCCACTCAAGCCCTCACTTCGCCCTTCAAGGATATGATCAACCAAGATCTTCTG	300
QY	101	GLYGLYValAsPlyshIsThrGlnPheTrparGlyTYrPhealaglysanleuAaserGly	120
Db	301	GGGGGGGTGGACAAAGCAACAGCATTCGTGAGATCTTGGGGCAACCTGGGCTTCGGC	360
QY	121	GLYAlaIaGlyValaIleThrSerLeuCySPheValTYrProLeuAsPheAlaArgThrArg	140
Db	361	GGTGGCGGGCGGCGCACTCCCTCTGTCTGTCTGGTACCGCGCTGATTTGGCAACACCGC	420
QY	141	LeuAlaIaAsPValGlyLySerGlyThrGlnValArgGluPheArgGlyLeuGlyAsPcys	160
Db	421	CTGGCAGCGAGCTGGGAAATCGACAGCACAGACCAGATTCCAGGCCCTGGAGACTCG	480
QY	161	LeuValIyssiIeThrLySerAspGlyIleahGlyLeuTYrGlnGlyIlePheSerValSer	180
Db	481	CTGGTGAAATGATCCAAAGTCGACGAGGATCGGGGGCTGTACAGGGCTTCATGTCTCC	540
QY	181	ValGlnGlyIleIleIleTYrArgAlaIaTYrPheGlyValTYrAspThrAlaIyGly	200
Db	541	GTCAGAGGCATCATCTATTACCGGGGGCTTACTTGGGGTATCGATACGGCCAAAGGC	600
QY	201	MeLeuProAsPProLyshsnThrHisIleValIaSerTTPmetIlealaglnThrVal	220
Db	601	ATGTCTCCCAACCCCAAGAACACCAACCATGTGTAGTGGATGATCGCAGACCGTG	660
QY	221	ThrAlaValAlaGlyValaIaSerTYrProPheAsPThrValaArgArgMetMetMet	240
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Db	721	CAGTCGGGGCGAAGAGACTACATCATGTACACAGCGGCAACGCTGATCTGTGAGAGAG	780
QY	261	IlePheArgAspIuIyGlyIyAlaIlePhePheLyGlyAlaIleProSerAsnValIleArg	280
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Db	841	GGCATGGGGGGCCCTTCGTGCTGTCTGTACGACGACACTCAAAAGATGATATC	894

US-09-810-644-3
; Sequence 3, Application US/09810644
; Patent No. US2002001292A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

Applicant:	Clevenger, William
Applicant:	Wiley, Sandra Elaine
Applicant:	Miller, Scott W.
Applicant:	Szabo, Tomas R.
Applicant:	Ghosh, Soumitra S.
Applicant:	Moos, Walter H.
Applicant:	Pel, Yashong
Title of Invention:	PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
File Reference:	NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
Current Application Number:	US/09/810,644
Current Filing Date:	2001-03-14
Number of SEQ ID NOS:	37
Software:	FASTSEQ for Windows Version 3.0
SEQ ID NO:	3
Length:	897
Type:	DNA
Organism:	Homo sapien
US-09-810-644-3	
Alignment Scores:	
Pred. NO:	2,32e-200
Score:	1543.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	100.00%
DB:	9
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QY	21 IleSerLystrAlaValAlaLaprolleGluArgValLysLeuLeuGlnValGlnHis 40
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QY	61 IleProLyGlnGlnGlyValIleSerPheTrpArgGlyAsnLeuAlaAsnValIleArg 80
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Db	241 TACTTCCCACTCAAGCCCTCACTTCGCTTCANAGATAGTCACAGCAAGATCTTCCTG 300
QY	101 GlyGlyValaAspLyHisIleThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSerGly 120
Db	301 GGGGGGCTGGAAACACACGCAAGTTCGGAAGTACTTTGGGGCAACCTGGCTCGGCG 360
QY	121 GlyAlaAlaGlyAlaThrSerIleCysPheValTyrProLeuAspPheAlaArgThrArg 140
Db	361 GGTGCGGCGGGGCACTCCCTCTCTCTCGTACGTCGCGCTGGATTTTCCAGAACCCGC 420
QY	141 LeuAlaAlaAspValGlyLysSerGlyTrpGlnArgGlnPheArgGlyLeuGlyAspCys 160
Db	421 CTGGCAGCGGAGCTGGAAAGTCCAGCAGACAGAGCCCGAGTCCGAGGCTGGGAATGCG 480
QY	161 LeuValLystrHisSerAspGlyIleArgGlyLeuTrpGlnGlyPheSerValSer 180
Db	481 CTGGTGAATGATCCCAATCCGAGGAGATCCGGGGCTGTACCGAGGCTTCAGTGTCTCC 540
QY	181 ValGlnGlyTleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200

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QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValaLeuArg 280
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RESULT 3

US-09-185-904A-3
Sequence 3, Application US/09185904A

Patent No. US20020177185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Willet, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLACATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 897
TYPE: DNA
ORGANISM: Homo sapien
US-09-185-904A-3

Alignment Scores:

Pred. No.: 2,32e-200 Length: 897
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-811-094-33 (1-298) x US-09-185-904A-3 (1-897)

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QY 21 IleSerLysThrAlaValaValaProIleGluArgValaLysLeuLeuGlnValaGlnHis 40
Db 61 ATCTCCAGAGCGGCGCGTGTGCGATCGAGCGGTCAGCTGCTGCTGCGAGGTCCAGAC 120
QY 41 AlaSerLysGlnIleAlaAlaAspLysGlyTrpLysGlyIleValaAspCysIleValaArg 60
Db 121 GCCAGCAAGCAGATCGCGCGCGCAAGACATACAAAGGCGATCGGACTCATGTCTCGCG 180
QY 61 IleProLysGlnGlnGlyValaLeuSerPheTrpArgGlyLysLeuAlaAsnValaIleArg 80
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Db 181 ATCCCAAGAGAGGCGGTCTGTCTCTTCTGTGAGGAGGCAACTTGCACACATTCATCCG 240
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
Db 241 TACTTCCCACTCAAGGCGCTCAACTTGTGCTTCAAGAGATAGTAAAGACAGATCTTCTCG 300
QY 101 GlyGlyValaAspLysHisThrGlnPheTrpArgGlyPheAlaGlyAsnLeuAlaSerGly 120
Db 301 GGGGGCGGTGACAAAGCAGACAGCGAGTCTTGAGGACTTTCGCGGCAACTCGGCTCCGCG 360
QY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValaTrpProLeuAspPheAlaArgTrpArg 140
Db 361 GGTGCGCGCGCGGACCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
QY 141 LeuAlaAlaAspValaGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
Db 421 CTGGCAGCGGACCGTGGGAAAGTACGACAGAGCGGACAGTTCGAGGCGCTGGAGACTTCC 480
QY 161 LeuValaLysIleThrLysSerAspGlyIleArgGlyLeuTrpGlnGlyPheSerValSer 180
Db 481 CTGGTGAAGATCAACCAAGTCCGACGCGATCCGGGGCGCTGTACACAGGCGCTTCACTGCC 540
QY 181 ValGlnGlyIleIleIleIleTrpArgAlaAlaValaValaValaValaValaValaVala 200
Db 541 GTCCAGGCGCATCATCTACCGGGGGGCTACTTGGCGCTGTACGATACGCGCAAGGC 600
QY 201 MetLeuProAspProLysAsnThrHisIleValaValSerTrpMetIleAlaGlnThrVal 220
Db 601 ATGCTCCCGACCGCCCAAGAACAGACATCGTGCGTGAATGATCGGCGAGACCGTGG 660
QY 221 ThrAlaValaAlaGlyValaValSerTrpProPheAspThrValaLarGargArGmetMet 240
Db 661 ACGGCGGTGGCGCGCTGTGTCTTACCCCTTCGACACGGTGGCGGCGCCATGATGATG 720
QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTrpThrGlyThrValaAspCysTrpArgLys 260
Db 721 CAGTCCGGCGGCAAGAGAGCTGACATCATGATACAGGCGACCGCTCGACTGTGAAGAG 780
QY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValaLeuArg 280
Db 781 ATCTTCAGAGATGAGGGGGGCGCAAGGCGCTTCTCAAGGTCGCGTGCACACGCTCTCGG 840
QY 281 GlyMetGlyGlyAlaPheValaLeuValaLeuValaLeuValaLeuValaValaIle 298
Db 841 GGCATGGGGGGCGCTTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 894
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RESULT 4

US-10-037-270-687
Sequence 687, Application US/10037270
Publication No. US20030104529A1
GENERAL INFORMATION:

APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyan
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yungang
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784CJP2B
CURRENT APPLICATION NUMBER: US/10/037, 270
CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
SOFTWARE: PL-FL-genes Version 1.0
SEQ ID NO: 687
LENGTH: 1212
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (131)..(1027)
US-10-037-270-687

Alignment Scores:
Pred. No.: 3,68e-200 Length: 1212
Score: 1543.00 Matches: 298
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

US-09-811-094-33 (1-298) x US-10-037-270-687 (1-1212)

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QY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 191 ATCTCCAAACGCGCGCTGGCTCCCATCGACGGGCTCAACCTGCTGCGAGCTCCAGCC 250
QY 41 AlaeSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 251 GCCAGCAACAGATCGCCGCGCAACAGCATCAACAGGCTCTGCACTGCTGCTCCG 310
QY 61 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 311 ATCCCAAGAGCAGGCGGTCTCTCTTGTGAGGGGCAACCTTGCCCAAGCTATTCGC 370
QY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
DB 371 TACTTCCCACTCAAGCCCTCACTGCTGCTCAAGATTAACAAACAGATCTCTG 430
QY 101 GlyGlyValAlaAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerGly 120
DB 431 GGGGCGCTGACACAGCAGCATCTCTGAGGACTTGGGGCAACCTGCTCCGCGC 490
QY 121 GlyAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThrArg 140
DB 491 GGTCCGCGCGCGCGCTCTCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 550
QY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 551 CTGGCAGCGGACGCTGGGAAAGTCAGCAGCAGGCGAGTCCAGGCTGGGAGACTGC 610
QY 161 LeuValLysIleThrLysSerAspCylLleArgLysLeuTyrGlnGlyPheSerValSer 180
DB 611 CTGTGTGAAGTCAACAGTCCAGCGCATCTGGGGCTGTACAGGGCTCCAGTGTCTCC 670
QY 181 ValGlnGlyIleIleIleIleTyrArgAlaAlaLysPheGlyValTyrAspThrAlaLysGly 200
DB 671 GTGCAGGGGATCATCTACCTACCGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 730
QY 201 MetLeuProAspProLysAsnThrHisIleValValSerTyrMetIleAlaGlnThrVal 220
DB 731 ATGCTCCCGCAACCCCAAGAACACGCAATCTGTGAGCTGATGATCCGAGACCTG 790
QY 221 ThrAlaValAlaGlyValValSerTyrProPheAspThrValArgTyrArgTyrMetMet 240
DB 791 ACGGCGCTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 850

QY 241 GlnSerGlyArgLysGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrPargLys 260
DB 851 CAGTCCGGCGCGCAAGAGCTGACATCATGTACAGGCGACCGTGCATGTTGGAGGAG 910
QY 261 IlePheArgAspGluGlyGlyAlaPhePheLysGlyAlaTyrPheAspValLeuArg 280
DB 911 ATCTCAGAGATGAGGGGCGCAAGCCCTTCTTACAGGCTGCTGCTGCTGCTGCTG 970
QY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 971 GGCATGGGGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1024

RESULT 5

US-10-044-090-152
Sequence 152, Application US/10044090
Publication No. US20020137081A1

GENERAL INFORMATION:

APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO: 152
LENGTH: 2592

TYPE: DNA
ORGANISM: Homo sapiens

FEATURE:
OTHER INFORMATION: Incyte ID No. US20020137081A1 1330214.11

NAME/KEY: misc.feature
LOCATION: 1131, 1929

OTHER INFORMATION: a, t, c, g, or other

US-10-044-090-152

Alignment Scores:
Pred. No.: 3,73e-195 Length: 2592
Score: 1510.00 Matches: 296
Percent Similarity: 99.33% Conservative: 2
Best Local Similarity: 98.67% Mismatches: 0
Query Match: 97.86% Indels: 2
DB: 13 Gaps: 0

US-09-811-094-33 (1-298) x US-10-044-090-152 (1-2592)

QY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyGlyIleAlaAla 20
DB 207 ATGACGGAACAGCCCATCTCTTCCCAAGACTTCTGGCCGGAGCATGCCGCGCC 266
QY 20 allelesThrAlaValAlaProIleGluArg-ValLysLeuLeuGlnValGlnHis 40
DB 267 CATCTCCAAAGCGCGCTGGCTCCGATCGACGGGCTCAACCTGCTGCTGCTGCTGCTG 326
QY 40 AlaeSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
DB 327 AGCCAGCAACAGATCGCCGCGCAACAGCATCAACAGGCTGCTGCTGCTGCTGCTG 386
QY 60 IleProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeuAlaAsnValIleArg 80
DB 387 GCATCCCAAGAGCAGGCGGTCTCTCTTGTGAGGGGCAACCTTGCCCAAGCTATTC 446
QY 80 rGlyThrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheL 100
DB 447 GCTACTTCCCACTCAACCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 506
QY 100 euGlyValAlaAspLysHisThrGlnPheTyrArgTyrPheAlaGlyAsnLeuAlaSerG 120
DB 507 TGGGGGCGCTGACAGCAGCAGGATCTGGAGTCTTTCGGCGCAACTGCTCCG 566
QY 120 LysIleAlaAlaGlyAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArgThr 140
DB 567 GCGTCCGCGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 626

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OY 140 rgleuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspC 160
DB 627 GCCTGGCAGCGAGCTGGGAAAGTCAGACAGACGGAGTCCGAGGCTTGGAGACT 686
OY 160 yslleuValLysIleThrLysSerAspGlyIleArgGlyLeuThrGlnGlyPheSerValS 180
DB 687 GCTTGTGTAAAGTACCAAGTCCAGGCAATCCGGGGCTGTACACGAGGCTTCAATGTCT 746
OY 180 erValGlnGlyIleIleThrLysArgAlaIleValPheGlyValTyrAspThrAlaLysG 200
DB 747 CCGTCAGAGCATCATCTACCCGGGGCTTCTTGGGCTGTACGATACGGCCAAAG 806
OY 200 lmetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrV 220
DB 807 GCATGCTCCCGACCCCAAGAACAGCAGCATCGTGTGAGCTGATGATCGCGCAGACCG 866
OY 220 alThrAlaValAlaGlyValValLysIleValSerTrpPheAspThrValArgAlaMetMetM 240
DB 867 TGACGGCCGTGGCCGGCTGTGTCTTACCCCTTGGACACGGTGGCGCGCATGATGA 926
OY 240 etGlnSerGlyArgLysGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgL 260
DB 927 TGACATCCGGCGCAAGAGCTGACATCATGTACACGGGCACTTCACCTTGTGAGGA 986
OY 260 ysllePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuA 280
DB 987 AGATCTCAGAGATGAGGGGGGCAAGCGCTTCTTCAAGGTCGTGTCACAGCTCAAGCTC 1046
OY 280 rglMetGlyGlyAlaPheValLeuValLeuValLeuValLeuValLysValIle 298
DB 1047 GGGGATGGGGGGCCCTTCTGTGTGTCTGTACAGAGCTCAAGAGGTGATC 1102

```

RESULT 6

```

US-09-811-094-2
; Sequence 2, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clewenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yezhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-811-094-2

```

Alignment Scores:

```

Pred. No.: 3,21e-188 Length: 897
Score: 1454.00 Matches: 274
Percent Similarity: 96.96% Conservative: 13
Best Local Similarity: 92.57% Mismatches: 9
Query Match: 94.23% Indels: 0
DB: 9 Gaps: 0

```

US-09-811-094-33 (1-298) x US-09-811-094-2 (1-897)

```

OY 1 MetThrGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
DB 1 ATGACAGATGCCGATGTCTTCCGCCAAGACTTCTGCGAGGTGGAGTGGCGCGAGCC 60

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OY 21 lIeSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
DB 61 ATCTCCAGAGCGCGGTAGCGCCCATCGAGCGGGTCAAGCTCTCTGAGGTGACAGAT 120
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnTrpLysGlyIleValAspCysIleValArg 60
DB 121 GCCACCAAGCAGATCACTGATTAAGCAATACAAAGGATATGAGCTGCTGCTCCGT 180
OY 61 lIeProLysGluGlnGlyValLeuSerPheTrpArgGlyAsnLeuAlaSerValIleArg 80
DB 181 ATTCACCAAGAGCAGAAAGTCTGTCTTGTGCGCGGTAACTGACCAATGTCAACAA 240
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTrpLysGlnIlePheLeu 100
DB 241 TACTTCCCAACCCAGGCTTTTAACTTCGCTTCAAGATTAATACAGACAGATCTTCCG 300
OY 101 GlyGlyValAspLysHisThrGlnPheTrpArgTrpPheAlaGlyAsnLeuAlaSerGly 120
DB 301 GGTGTGTGGACAAAGAAACCAAGTTTGGCCCTTACTTGGCAGAGGATCTGCAATCG 360
OY 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
DB 361 GGTGCCGCGAGGGCCACATCCCTGTGTTTGTGTMCCCTTGATTTTCCCGTACCCGT 420
OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 421 CTACAGAGCTGATGGGTAAAGCTGAGCTGAAAGGAATTCGAGCGCTGTGATCTGC 480
OY 161 LeuValLysIleThrLysSerAspGlyIleArgGlyLeuThrGlnGlyPheSerValSer 180
DB 481 CTGGTTAAGATCTACAAATCTATGATTAAGGGGCTGTACCAAGGCTTTAACTGTCT 540
OY 181 ValGlnGlyIleIleThrLysArgAlaIleValPheGlyValTyrAspThrAlaLysGly 200
DB 541 GTGCAGGATATATCTTACCGAGCGGCTTCTGTGTATATATACCTCAAGAGGA 600
OY 201 MetLeuProAspProLysAsnThrHisIleValValSerTrpMetIleAlaGlnThrVal 220
DB 601 ATGCTTCCGAGTCCCAAGAACTGACATCATCGATCATGATGATGATCCACAGACTGTC 660
OY 221 ThrAlaValAlaGlyValValSerTrpPheAspThrValArgArgMetMetMet 240
DB 661 ACTGCTGTGGCCGGGTGACTTCTTATTCATTTGACACCGCTTCGCCGCGCATGATGATG 720
OY 241 GlnSerGlyArgLysGlyAlaAspIleMetTrpThrGlyThrValAspCysTrpArgLys 260
DB 721 CAGTCAGGCGCAAGAACTGACATCATGTACACAGGCACTGACTGTGCGGGAAG 780
OY 261 lIePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
DB 781 ATTGCTCGTGAAGAGGAGCAAGCTTTTCAAGGGGTCGATGCAATGATGTCTCACA 840
OY 281 GlyMetGlyGlyAlaPheValLeuValLeuValTyrAspGluLeuLysLys 296
DB 841 GGCATGGGTGTCTTGTGTCTGTGTATGATGAATCAAGAG 888

```

RESULT 7

```

US-09-810-644-2
; Sequence 2, Application US/09810644
; Patent No. US2002001292A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clewenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yezhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/810,644
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 897
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-810-644-2

```

FILE REFERENCE: 660088.420D3
 CURRENT APPLICATION NUMBER: US/09/810.644
 CURRENT FILING DATE: 2001-03-14
 NUMBER OF SEQ ID NOS: 37
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 897
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-810-644-2

Alignment Scores:
 Pred. No.: 3 21e-188
 Score: 1454.00
 Percent Similarity: 96.96%
 Best Local Similarity: 92.57%
 Query Match: 94.23%
 Gaps: 0

US-09-811-094-33 (1-298) x US-09-810-644-2 (1-897)

QY 1 MethrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 1 ATGACAGATGCGCATGTCCTTCCGCAAGACTCTCGCAGGTGAGTGCAGCCAGCC
 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 61 ATCTCCAGAGCGGGGAGGCGCCATCGAGCGGGTCAAGCTGCTGCGAGGTGAGCAT 120
 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 121 GCCACAGACAGATCACTGCAGATTAAGCAATCAAGCATTAAGCTCGCTCGCT 180
 61 IleProLysGluGlnGlyValIleSerPheTrpArgLysLeuAlaAsnValIleArg 80
 181 ATTCCCAAGAGAGCAAGAAATTCTGCTCTTGGCGCGGTAACTCGCAATGTCAACAGA 240
 81 TyrPheProThrGlnAlaIleAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 241 TACTTCCGACCGAGGCTTAACTTGCCTTCAAAAGTAATACAGAGATCTTCCG 300
 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyIleAlaAlaSerGly 120
 301 GGTGGTGTGACAGACAGAACCCAGTTTGGCGCTACTTGGCGGAACTCGCATCGGGT 360
 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 361 GGTGCGGAGGGGACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgLysPheArgGlyIleGlyAspCys 160
 421 CTGACAGCTGATGTGGTAAAGCTGAGCTGAAAGGAAATTCGAGGCTCGGTGACTGG 480
 161 LeuValLysIleThrLysSerAspGlyIleArgLysLeuTyrGlnGlyIlePheSerValSer 180
 481 CTGCTTAACATCTACAAATGTGATGAGTAAAGCTGCTTACCAAGGCTTAAAGCTTCT 540
 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
 541 GTGACAGGTATATCATCTACCGAGCGCTACTTGGGTATCATAGACATGCAAGGGA 600
 201 MetLeuProAspProLysAsnThrHisIleValIleSerTrpMetIleAlaGlnThrVal 220
 601 ATGCTTCCGATCCCAAGACACTACATCATCATCATCATCATCATCATCATCATCAT 660
 221 ThrAlaValAlaGlyValAlaSerTyrProPheAspThrValArgArgMetMetMet 240
 661 ACTGCTCTTCCGCGGTGACTTCTCATCATCATCATCATCATCATCATCATCATCAT 720
 241 GlnSerGlyArgGlyValAlaAspIleMetTyrThrGlyThrValAspCysTrpArgLys 260
 721 CAGTCAGGGGCGCAAGAGACTGATCATCTGTACACAGGACGCTGTGACGCGGGAG 780

QY 261 IlePheArgAspGluGlyIleLysAlaPhePheLysGlyAlaTrpSerAsnValIleArg 280
 781 ATTGCTCGGATGAGAGAGCAAGGCTTTTCAAGGCTGATGATGATGATGATGATGAT 840
 QY 281 GlyMetGlyGlyAlaPheValIleValIleValTyrAspGluLeuLysLys 296
 841 GCGATGCGTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCTTGTGCT 888

RESULT 8
 US-09-185-904A-2
 Sequence 2, Application US/09185904A
 Patent No. US20020177185A1

GENERAL INFORMATION:
 APPLICANT: Anderson, Christen M.
 APPLICANT: Davis, Robert E.
 APPLICANT: Clevenger, William
 APPLICANT: Wiley, Sandra Eileen
 APPLICANT: Willet, Scott W.
 APPLICANT: Szabo, Tomas R.
 APPLICANT: Ghosh, Soumitra S.
 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
 TITLE OF INVENTION: THEREFOR
 FILE REFERENCE: 660088.420
 CURRENT APPLICATION NUMBER: US/09/185.904A
 CURRENT FILING DATE: 1998-11-03
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO 2
 LENGTH: 897
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-185-904A-2

Alignment Scores:
 Pred. No.: 3 21e-188
 Score: 1454.00
 Percent Similarity: 96.96%
 Best Local Similarity: 92.57%
 Query Match: 94.23%
 Gaps: 0

US-09-811-094-33 (1-298) x US-09-185-904A-2 (1-897)

QY 1 MethrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
 1 ATGACAGATGCGCATGTCCTTCCGCAAGACTCTCGCAGGTGAGTGCAGCCAGCC
 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGlnHis 40
 61 ATCTCCAGAGCGGGGAGGCGCCATCGAGCGGGTCAAGCTGCTGCGAGGTGAGCAT 120
 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleValArg 60
 121 GCCACAGACAGATCACTGCAGATTAAGCAATCAAGCATTAAGCTCGCTCGCT 180
 61 IleProLysGluGlnGlyValIleSerPheTrpArgLysLeuAlaAsnValIleArg 80
 181 ATTCCCAAGAGAGCAAGAAATTCTGCTCTTGGCGCGGTAACTCGCAATGTCAACAGA 240
 81 TyrPheProThrGlnAlaIleAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
 241 TACTTCCGACCGAGGCTTAACTTGCCTTCAAAAGTAATACAGAGATCTTCCG 300
 101 GlyGlyValAspLysHisThrGlnPheTrpArgTyrPheAlaGlyIleAlaAlaSerGly 120
 301 GGTGGTGTGACAGACAGAACCCAGTTTGGCGCTACTTGGCGGAACTCGCATCGGGT 360
 121 GlyAlaAlaGlyAlaThrSerLeuCysPheValTyrProLeuAspPheAlaArgThrArg 140
 361 GGTGCGGAGGGGACATCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgLysPheArgGlyIleGlyAspCys 160


```

; Sequence 13437, Application US/10198846
; Publication No. US2003009974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Mang, Youzhen
; APPLICANT: Steinhmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRL-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIORITY FILING DATE: 2002-07-18
; PRIORITY FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13437
; LENGTH: 1711
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1, 2, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405,
; LOCATION: 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415,
; LOCATION: 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425,
; LOCATION: 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444,
; LOCATION: 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454,
; OTHER INFORMATION: n = A,T,C or G
; US-10-198-846-13437

Alignment Scores:
Pred. No.: 1,19e-181 Length: 1711
Score: 1409.00 Matches: 263
Percent Similarity: 94.63% Conservative: 19
Best Local Similarity: 88.26% Mismatches: 16
Query Match: 91.32% Indels: 0
Gaps: 0
DB: 14

US-09-811-094-33 (1-298) x US-10-198-846-13437 (1-1711)
OY 1 MetThGluGlnAlaIleSerPheAlaLysAspPheAlaGlyGlyIleAlaAla 20
DB 167 ATGGGTGATCAGCGCTGGAGCTTCCCTAAAGAGCTTCTGCGCGGCGCTCCGCC 226
OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnAlaHis 40
DB 227 GTCTCCAAAGCCGCGCTGCGCCCATGAGAGGCTCAAACTGCTGCTGAGTCAAGC 286
OY 41 AlaserLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleVal 60
DB 287 GCCAGCAACAGATCAGTGCAGACAGACATCAAGAGGATCATGATGCTGTGAGA 346
OY 61 ILPProLysGluGlnIleValLeuSerPheTrpArgLysAlaLeuAlaValIleArg 80
DB 347 ATCCCTAAGAGCAGGCGCTTCTCTCTCTGAGGGGAGGAGGAGGAGGAGGAGG 406
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePhe 100
DB 407 TATCTCCCAACCAAGCTCACTCACTTGCCTCAAGAGCACTACACAGCACTCTCT 466
OY 101 GlyAlaValAspLysAlaThrGlnPheTrpArgTyrPheAlaGlyAsnLeuAlaSer 120
DB 467 GGGGGGTGATGCGCATACAGCACTTCTGCGCTATTTGCGTGAACCTGGGCTCG 526
OY 121 GlyAlaValAspLysAlaThrSerLeuGlyPheValTyrProLeuAspPheAlaArg 140
DB 527 GGGGGCGGTGGGGCCACCTCCCTTGTGCTTGTCTACCCGCTGGACTTGTGAGAC 586

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OY 141 LeuAlaAlaAspValGlyLysSerGlyThrGluArgGluPheArgGlyLeuGlyAspCys 160
DB 587 TTGGCTGCTGATGTCGGCAGAGGGGCGCGCCAGCAGTCAATTCAGTGTGGGAGCTGT 646
OY 161 LeuValLysIleThrLysSerAspGlyIleArgLysLeuTyrGlnGlyPheSerValSer 180
DB 647 ATCTCAAGATCTTCAAGCTGATGCTGCTGAGGGGCTTACAGGCTTCAAGCTCTCT 706
OY 181 ValGlnGlyIleIleIleTyrArgAlaAlaTyrPheGlyValTyrAspThrAlaLysGly 200
DB 707 GTCCAGGCACTCATATATATATATATATATATATATATATATATATATATATATAT 766
OY 201 MetLeuProAspProLysAsnThrHisIleValAlaSerTrpMetIleAlaGlnThrVal 220
DB 767 ATGCTGCTGAGCCCAAGAGAGTGTGCTGAGCTGAGTGTGAGTGTGAGTGTGAGTGT 826
OY 221 ThrAlaValAlaGlyValAlaValSerTyrPheAspThrValArgArgArgMetMet 240
DB 827 ACAGCAGTCCAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 886
OY 241 GlnSerGlyArgLysGlyAlaAspIleMetLysThrGlyThrValAspCysArgLys 260
DB 887 CAGTCCGCGGAGAGAGGCGCGCTATATATATATATATATATATATATATATATATAT 946
OY 261 IlePheArgAspGluGlyLysAlaPhePheLysGlyAlaTrpSerAsnValLeuArg 280
DB 947 ATTCAGAAAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1006
OY 281 GlyMetGlyGlyAlaPheValLeuValLeuTyrAspGluLeuLysValIle 298
DB 1007 GCATGCGCGCGCTCTTGTATGCTGTGTATGATGATGATGATGATGATGATGATG 1060

RESULT 11
US-09-811-094-1
; Sequence 1, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Cleveland, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Fel, Yezhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.42004
; CURRENT APPLICATION NUMBER: US/09/811,094
; PRIORITY FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 894
; LENGTH: 894
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-811-094-1

Alignment Scores:
Pred. No.: 7.07e-179 Length: 894
Score: 1385.50 Matches: 260
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 87.25% Mismatches: 16
Query Match: 89.79% Indels: 1
Gaps: 1
DB: 9

US-09-811-094-33 (1-298) x US-09-811-094-1 (1-894)
OY 1 MetThGluGlnAlaIleSerPheAlaLysAspPheAlaGlyGlyIleAlaAla 20
DB 1 ATGGGTGATCAGCGCTGGAGCTTCCCTAAAGAGCTTCTGCGCGGCGCTCCGCC 60

```



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Db 778 ATTGCAAAAGCAGAGGAGCCAGGCTCTTCAAGGCTGGTCCATGCTGAC 837
OY 281 GYMeTgLyglYAlaPheValLeuValLeuTyrAspGluLeuYsLyValIle 298
Db 838 GGCATGGCGGCTCTTTGTATTGGTGTGATGATGATCAAAATATGTC 891

RESULT 13
US-09-185-904A-1
Sequence 1, Application US/09185904A
Patent No. US2002017185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Cleveland, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185, 904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 894
TYPE: DNA
ORGANISM: Homo sapien
US-09-185-904A-1

Alignment Scores:
Pred. No.: 7,07e-179 Length: 894
Score: 1385.50 Matches: 260
Percent Similarity: 94.30% Conservative: 21
Best Local Similarity: 87.25% Mismatches: 16
Query Match: 89.79% Gaps: 1

US-09-811-094-33 (1-298) x US-09-185-904A-1 (1-894)
OY 1 MetThrGluGlnAlaIleSerPheAlaLysAspPheLeuAlaGlyIleAlaAla 20
Db 1 ATGGGTGATCAGCGCTGGAGCTCTTAAGGACTTCTGGCGGGCGGCTGGCG 60
OY 21 IleSerLysThrAlaValAlaProIleGluArgValLysLeuLeuGlnValGln 40
Db 61 GTCTCCAAAGACCGCGCTGCCCATCGAGAGGCTCAAACTCTCTCAGGTCAC 120
OY 41 AlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleValAspCysIleVal 60
Db 121 GCCAGCAAAACAGTACAGTGCAGAACAGTACAAAGGATCATGATTGCTGAGA 180
OY 61 IleProLysGluGlnGlyValIleLeuSerPheTyrArgGlyAsnLeuAlaAsnValIle 80
Db 181 ATCCCTTAAGACAGAGGCTTCTCTCTTGGAGGGGTAACCTGGCCACGTAATCG 240
OY 81 TyrPheProThrGlnAlaLeuAsnPheAlaPheLysAspLysTyrLysGlnIlePheLeu 100
Db 241 TACTTCCCAACCCAGCTCTCACTTCGCTCAAGCAAGCAAGTACAAACAGCTCTTCTTA 300
OY 101 G1Yg1YVa1AspLyAlaPheValLeuValLeuTyrAspGluLeuYsLyValIle 120
Db 301 GGGGGTGTGGATCGCATAGCAGTCTGGCGCTACTTGTGCTGTAACCTGGCGTGG 360
OY 121 G1YAla1Ag1YAlaThrSerLeuCyAPheValTyrProLeuAspPheAlaArgThrArg 140
Db 361 GGGGGCGGTGGGGCCACCTCCCTTGGTGTGTACCCCTGAGACTTGTCTAGGCAAG 420
OY 141 LeuAla1AspValG1YLySerG1YThrG1uArgG1uPheArgG1YLeuG1YAspCys 160

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Db 421 TTGGCTCTGATGTGGCGAGGCC---GCCAGCGTGAATTCATGCTGCGGCGACTGT 477
OY 161 LeuValYsIleLeuThrLysSerAspGlyIleArgGlyLeuYsLyValIlePheSerValSer 180
Db 478 ATCATCAAGATCTTCAAGTCTATGCTGATGCGGTGAGGGGCTTACCAAGGTTTCAGCTCTCT 537
OY 181 ValGlnGlyIleIleLeuThrArgAlaIlePheGlyValIleYsAspThrAlaLysGly 200
Db 538 GTCCAGGCACTATTCATATGATGACCTCTTCCGAGTCTATGATCTCCCAAGGGG 597
OY 201 MetLeuProAspProLysAsnThrHisIleValIleValIleSerPheIleAlaGlnThrVal 220
Db 598 ATCTGCTTACCCCAAGAACCTGCACATTTTGTGAGCTGATGATTCGCCAGAGTGTG 657
OY 221 ThrAlaValAlaGlyValAlaIleSerTyrProPheAspThrValArgArgMetMet 240
Db 658 ACGGCACTGCGAGGCGCTGCTGCTACCCCTTGACACTGCTGCTGATGATGATGATG 717
OY 241 GlnSerGlyArgGlyGlyAlaAspIleMetTyrThrGlyThrValAspCysTyrArgLys 260
Db 718 CAGTCCGGCGGGAAGGGCCGATATATGATACAGGGGACAGTGTGCTGAGAGAG 777
OY 261 IlePheArgAspGluGlnGlyLysAlaPhePheGlyValAlaTyrSerAsnValLeuArg 280
Db 778 ATTGCAAAAGCAGAGGAGCCAGGCTCTTCAAGGTCGCTGCTCAATGCTGAGAG 837
OY 281 GYMeTgLyglYAlaPheValLeuValLeuTyrAspGluLeuYsLyValIle 298
Db 838 GGCATGGCGGCTCTTTGTATTGGTGTGATGATGATCAAAATATGTC 891

RESULT 14
US-09-969-708-213
Sequence 213, Application US/09969708
Patent No. US20020102532A1
GENERAL INFORMATION:
APPLICANT: Anagnostis, Meena
APPLICANT: Anagnostis, Meena
TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Sign
FILE REFERENCE: 689290-70
CURRENT APPLICATION NUMBER: US/09/969, 708
CURRENT FILING DATE: 2001-10-03
PRIOR APPLICATION NUMBER: US/60/237,606
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: US/60/237,608
PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 425
SOFTWARE: Pileupin Version 3.0
SEQ ID NO 213
LENGTH: 1116
TYPE: DNA
ORGANISM: Homo sapiens
US-09-969-708-213

Alignment Scores:
Pred. No.: 8.96e-175 Length: 1116
Score: 1356.50 Matches: 260
Percent Similarity: 99.24% Conservative: 1
Best Local Similarity: 99.66% Mismatches: 1
Query Match: 87.91% Gaps: 1

US-09-811-094-33 (1-298) x US-09-969-708-213 (1-1116)
OY 36 LeuGlnValAlaGlnHisAlaSerLysGlnIleAlaAlaAspLysGlnTyrLysGlyIleVal 55
Db 1 CTGCAAGTCCACAGCCAGCAGCAAGTACGCGCGGAGCAAGCAATGATCAAGGCTATCG 60
OY 56 AspCysIleValAlaG1YLeuProLysGluGlnGlyValLeuSerPheTyrArgGlyAsnLeu 75
Db 61 GACTGATTGTCCGATCCCAAGAGCAAGGCGCTGTCTCTCTGAGGGCAACTT 120

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